

SEQUENCE LISTING

<110> BASF AG

<120> Process for the production of sulfur-containing fine chemicals

<130> M/43128

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 1317

<212> DNA

<213> Corynebacterium diphtheriae

<220>

<221> CDS

<222> (1)..(1317)

<223>

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Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ser Asp Thr Ser Ala
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cgc aac cta ccg att tac ctg aca tca tcg tac gtt ttt aat gac gcc 144
Arg Asn Leu Pro Ile Tyr Leu Thr Ser Ser Tyr Val Phe Asn Asp Ala
35 40 45
gaa cac gca gca aac cgc ttc aac ctt tcc gac gcc ggc ccg gtt tac 192
Glu His Ala Ala Asn Arg Phe Asn Leu Ser Asp Ala Gly Pro Val Tyr
50 55 60
tct cgc ctg acc aac cca act gtc gcg gca gtc gaa gaa cgc cta gcc 240
Ser Arg Leu Thr Asn Pro Thr Val Ala Ala Val Glu Glu Arg Leu Ala
65 70 75 80
aat ctt gaa ggt ggc gta cac gcc gta ctt ttc gct tcc gga atg gcc 288
Asn Leu Glu Gly Gly Val His Ala Val Leu Phe Ala Ser Gly Met Ala
85 90 95

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gtg tcc agt cct cgc att tac ggc ggc acc gaa aca ctc ttt gcc gtc Val Ser Ser Pro Arg Ile Tyr Gly Gly Thr Glu Thr Leu Phe Ala Val 115 120 125	384
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gac cca gcc tca tgg gag gct gca gtt caa gac aac acg gta gct ctc Asp Pro Ala Ser Trp Glu Ala Ala Val Gln Asp Asn Thr Val Ala Leu 145 150 155 160	480
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gcc aac cac gag aaa gta gcc aag gtt aac tac gca ggc ctt ccc gac Ala Asn His Glu Lys Val Ala Lys Val Asn Tyr Ala Gly Leu Pro Asp 325 330 335	1008
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<211> 438

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<213> Corynebacterium diphtheriae

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Glu His Ala Ala Asn Arg Phe Asn Leu Ser Asp Ala Gly Pro Val Tyr 50 55 60
Ser Arg Leu Thr Asn Pro Thr Val Ala Ala Val Glu Glu Arg Leu Ala 65 70 75 80
Asn Leu Glu Gly Gly Val His Ala Val Leu Phe Ala Ser Gly Met Ala 85 90 95
Ala Glu Thr Ala Ala Ile Leu Asn Ile Ala Arg Ala Gly Ser His Ile 100 105 110
Val Ser Ser Pro Arg Ile Tyr Gly Gly Thr Glu Thr Leu Phe Ala Val 115 120 125

Thr	Leu	Ala	Arg	Leu	Gly	Ile	Glu	Thr	Thr	Phe	Val	Glu	Asn	Pro	Asp	130	135	140
Asp	Pro	Ala	Ser	Trp	Glu	Ala	Ala	Val	Gln	Asp	Asn	Thr	Val	Ala	Leu	145	150	155
Tyr	Gly	Glu	Thr	Phe	Ala	Asn	Pro	Gln	Ala	Asp	Val	Leu	Asp	Ile	Pro	165	170	175
Ala	Ile	Ala	Glu	Val	Ala	His	Lys	His	Gln	Val	Pro	Leu	Ile	Val	Asp	180	185	190
Asn	Thr	Leu	Ala	Thr	Ala	Ala	Leu	Val	Arg	Pro	Leu	Glu	Leu	Gly	Ala	195	200	205
Asp	Val	Val	Val	Ala	Ser	Leu	Thr	Lys	Phe	Tyr	Thr	Gly	Asn	Gly	Ser	210	215	220
Gly	Leu	Gly	Gly	Val	Leu	Ile	Asp	Gly	Gly	Asn	Phe	Asp	Trp	Thr	Val	225	230	235
Thr	Arg	Asn	Gly	Glu	Pro	Ile	Phe	Pro	Asp	Phe	Val	Thr	Pro	Asp	Pro	245	250	255
Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ser	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	260	265	270
Leu	Lys	Ala	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ala	Ala	Pro	Ser	275	280	285
Pro	Leu	Asn	Ala	Trp	Ile	Thr	Ala	Gln	Gly	Leu	Asp	Thr	Leu	Ser	Leu	290	295	300
Arg	Val	Gln	Arg	His	Asn	Glu	Asn	Ala	Leu	Ala	Val	Ala	Gln	Phe	Leu	305	310	315
Ala	Asn	His	Glu	Lys	Val	Ala	Lys	Val	Asn	Tyr	Ala	Gly	Leu	Pro	Asp	325	330	335
Ser	Pro	Trp	Tyr	Pro	Val	Lys	Glu	Lys	Leu	Gly	Phe	Asp	Tyr	Thr	Gly	340	345	350
Ser	Val	Leu	Ser	Phe	Asp	Val	Lys	Gly	Gly	Lys	Asn	Glu	Ala	Trp	Arg	355	360	365
Phe	Ile	Asp	Ala	Leu	Lys	Leu	His	Ser	Asn	Leu	Ala	Asn	Val	Gly	Asp	370	375	380
Val	Arg	Ser	Leu	Val	Val	His	Pro	Ala	Thr	Thr	Thr	His	Ser	Gln	Ser	385	390	395

Glu Glu Ser Ala Leu Leu Ala Ala Gly Ile Asn Gln Ala Thr Ile Arg
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Ala Gly Phe Asp Ala Ile
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<213> Mycobacterium tuberculosis

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<222> (1)..(1350)

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 Ser Phe Glu Thr Lys Gln Ile His Ala Gly Gln His Pro Asp Pro Thr
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 Thr Asn Ala Arg Ala Leu Pro Ile Tyr Ala Thr Thr Ser Tyr Thr Phe
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gac gac acc gcg cac gcc gcc gcc ctg ttc gga ctg gaa att ccg ggc 192
 Asp Asp Thr Ala His Ala Ala Ala Leu Phe Gly Leu Glu Ile Pro Gly
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aat atc tac acc cgg atc ggc aac ccc acc acc gac gtc gtc gag cag 240
 Asn Ile Tyr Thr Arg Ile Gly Asn Pro Thr Thr Asp Val Val Glu Gln
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 85 90 95

ggg cag gcc gcg gag acg ttc gcc atc ttg aac ctg gcc ggc gcg ggc 336
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 Asp His Ile Val Ser Ser Pro Arg Leu Tyr Gly Gly Thr Tyr Asn Leu
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                        405                        410                        415

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                        420                        425                        430

ttt gcc gcg gcc cgc aga ttc agc gcc gac ccg cag tcc gtg gcg gcg      1344
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Phe                                                                1350

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<213> Mycobacterium tuberculosis

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Asn Ile Tyr Thr Arg Ile Gly Asn Pro Thr Thr Asp Val Val Glu Gln
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Arg Ile Ala Ala Leu Glu Gly Gly Val Ala Ala Leu Phe Leu Ser Ser
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Gly Gln Ala Ala Glu Thr Phe Ala Ile Leu Asn Leu Ala Gly Ala Gly
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Asp His Ile Val Ser Ser Pro Arg Leu Tyr Gly Gly Thr Tyr Asn Leu
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Phe His Tyr Ser Leu Ala Lys Leu Gly Ile Glu Val Ser Phe Val Asp
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Asp Pro Asp Asp Leu Asp Thr Trp Gln Ala Ala Val Arg Pro Asn Thr

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His	Gly	Val	Val	Phe	Ala	Glu	Leu	Gly	Pro	Pro	Ala	Phe	Ala	Leu	Lys
			260					265					270		
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Arg	Asp	Asp	Val	Leu	Ser	Val	Asn	Tyr	Ala	Gly	Leu	Pro	Ser	Ser	Pro
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Trp	His	Glu	Arg	Ala	Lys	Arg	Leu	Ala	Pro	Lys	Gly	Thr	Gly	Ala	Val
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Ser	Leu	Val	Ile	His	Pro	Ala	Ser	Thr	Thr	His	Ala	Gln	Leu	Ser	Pro
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Ala	Glu	Gln	Leu	Ala	Thr	Gly	Val	Ser	Pro	Gly	Leu	Val	Arg	Leu	Ala
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<211> 1284

<212> DNA

<213> Clostridium acetobutylicum

<220>

<221> CDS

<222> (1)..(1284)

<223>

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caa aca aca tca tat gta ttt aaa aat gct gat cat gca gca aat tta 144
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 35 40 45

ttt caa ttg aaa gaa cct gga aat gta tat aca agg ata atg aat cca 192
 Phe Gln Leu Lys Glu Pro Gly Asn Val Tyr Thr Arg Ile Met Asn Pro
 50 55 60

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gct gga ctt gca aca gca tca gga ctt gca gca att acc tat gct att 288
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tta aat gtg gca agt gct ggg gat gaa att gtt gca gca agt acc tta 336
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 100 105 110

tat ggt gga aca tat gaa tta ttt ggg gtt act ctt aag aag ctt gga 384
 Tyr Gly Gly Thr Tyr Glu Leu Phe Gly Val Thr Leu Lys Lys Leu Gly
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gaa gct ggt aaa aga ttt ata aat agt gtt aaa cta ttc tct ctt ttg Glu Ala Gly Lys Arg Phe Ile Asn Ser Val Lys Leu Phe Ser Leu Leu 355 360 365			1104
gca aat gtt gca gat gca aaa tca ctt gtt ata cat cct tca agt aca Ala Asn Val Ala Asp Ala Lys Ser Leu Val Ile His Pro Ser Ser Thr 370 375 380			1152
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cca gat atg ata aga ctt tca ata gga gta gag gat gca gag gat tta			1248

Pro Asp Met Ile Arg Leu Ser Ile Gly Val Glu Asp Ala Glu Asp Leu
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1284

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<211> 427

<212> PRT

<213> Clostridium acetobutylicum

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 50 55 60

Thr Thr Asp Val Phe Glu Gln Arg Val Ala Ala Leu Glu Gly Gly Val
 65 70 75 80

Ala Gly Leu Ala Thr Ala Ser Gly Leu Ala Ala Ile Thr Tyr Ala Ile
 85 90 95

Leu Asn Val Ala Ser Ala Gly Asp Glu Ile Val Ala Ala Ser Thr Leu
 100 105 110

Tyr Gly Gly Thr Tyr Glu Leu Phe Gly Val Thr Leu Lys Lys Leu Gly
 115 120 125

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 130 135 140

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260 265 270

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275 280 285

Glu Ser Leu Ser Leu Arg Val Gln Lys His Val Asp Asn Thr Arg Lys
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340 345 350

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370 375 380

Thr His Ala Glu Leu Asn Glu Glu Glu Gln Lys Ala Ala Gly Val Thr
385 390 395 400

Pro Asp Met Ile Arg Leu Ser Ile Gly Val Glu Asp Ala Glu Asp Leu
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Ile Trp Asp Leu Asn Gln Ala Leu Glu Gln Ala
420 425

<210> 7

<211> 1293

<212> DNA

<213> Bacillus halodurans

<220>

<221> CDS

<222> (1)..(1293)

<223>

<400> 7

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gga cag gag atc gat ccg aca acg ttg tcg cga gcc gtc cca ttg tac	96
Gly Gln Glu Ile Asp Pro Thr Thr Leu Ser Arg Ala Val Pro Leu Tyr	
20 25 30	
caa acg acg tcc tac gga ttt aaa gat aca gac cat gcg gcg aat tta	144
Gln Thr Thr Ser Tyr Gly Phe Lys Asp Thr Asp His Ala Ala Asn Leu	
35 40 45	
ttt tca cta agt gaa ttt ggc aat atc tat acc cga ttg atg aac cca	192
Phe Ser Leu Ser Glu Phe Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro	
50 55 60	
acg aca gat gtg ttt gaa aaa cgt gtg gct gcg tta gaa gga gga gcg	240
Thr Thr Asp Val Phe Glu Lys Arg Val Ala Ala Leu Glu Gly Gly Ala	
65 70 75 80	
gca gct tta gcg acg gcc tca ggg cag gcg gcc att acg tat tcg att	288
Ala Ala Leu Ala Thr Ala Ser Gly Gln Ala Ala Ile Thr Tyr Ser Ile	
85 90 95	
tta aat att gcg gag gct gga gat gaa atc gtg tcc gct agt agc ctt	336
Leu Asn Ile Ala Glu Ala Gly Asp Glu Ile Val Ser Ala Ser Ser Leu	
100 105 110	
tac ggc gga acg tat aat tta ttt tcg att acg ttg cca aag cta ggg	384
Tyr Gly Gly Thr Tyr Asn Leu Phe Ser Ile Thr Leu Pro Lys Leu Gly	
115 120 125	
gta aac gtc cgt ttc gtt gat cca tcg gac cca gaa aac ttc aaa gca	432
Val Asn Val Arg Phe Val Asp Pro Ser Asp Pro Glu Asn Phe Lys Ala	
130 135 140	
gcg att act gaa aag acg aaa gcc att ttc gct gag tcg att gga aac	480
Ala Ile Thr Glu Lys Thr Lys Ala Ile Phe Ala Glu Ser Ile Gly Asn	
145 150 155 160	
cct aag gga gac gtg tta gat att gaa gcg gtg gcg aaa gtt gca cac	528
Pro Lys Gly Asp Val Leu Asp Ile Glu Ala Val Ala Lys Val Ala His	
165 170 175	
gat cat cac ctt ccc ctc att gtc gat aac acg ttt cca agc cca tat	576
Asp His His Leu Pro Leu Ile Val Asp Asn Thr Phe Pro Pro Tyr	
180 185 190	
ttg ctt caa ccg ata aag cac ggc gca gac att gtt gtg cat tca gca	624
Leu Leu Gln Pro Ile Lys His Gly Ala Asp Ile Val Val His Ser Ala	
195 200 205	

aca	aaa	ttt	atc	ggt	ggt	cat	ggg	acg	tcg	ata	gga	ggg	atc	att	gtc	672
Thr	Lys	Phe	Ile	Gly	Gly	His	Gly	Thr	Ser	Ile	Gly	Gly	Ile	Ile	Val	
210						215					220					
gat	gga	ggg	acg	ttt	gat	tgg	gcg	aaa	acg	gat	cga	tat	cca	ggg	cta	720
Asp	Gly	Gly	Thr	Phe	Asp	Trp	Ala	Lys	Thr	Asp	Arg	Tyr	Pro	Gly	Leu	
225					230					235					240	
aca	aca	cct	gat	ccg	agt	tac	cac	ggt	gtt	gta	tat	aca	gat	gcg	gtc	768
Thr	Thr	Pro	Asp	Pro	Ser	Tyr	His	Gly	Val	Val	Tyr	Thr	Asp	Ala	Val	
				245				250						255		
ggt	cca	att	gct	tat	att	att	aaa	gcg	cgt	gtt	cag	cta	ttg	cgt	gac	816
Gly	Pro	Ile	Ala	Tyr	Ile	Ile	Lys	Ala	Arg	Val	Gln	Leu	Leu	Arg	Asp	
			260					265					270			
atg	ggg	gca	gcc	ata	tcg	cca	ttt	aac	tcg	ttt	tta	ctg	ttg	caa	ggg	864
Met	Gly	Ala	Ala	Ile	Ser	Pro	Phe	Asn	Ser	Phe	Leu	Leu	Leu	Gln	Gly	
		275					280					285				
ttg	gaa	acg	ttg	cat	tta	cgg	atg	gag	aga	cat	agt	gaa	aat	gcc	tac	912
Leu	Glu	Thr	Leu	His	Leu	Arg	Met	Glu	Arg	His	Ser	Glu	Asn	Ala	Tyr	
	290					295					300					
aaa	gta	gca	gag	ttc	ctt	gag	caa	cat	caa	gcg	gtc	gaa	tcg	gtg	agc	960
Lys	Val	Ala	Glu	Phe	Leu	Glu	Gln	His	Gln	Ala	Val	Glu	Ser	Val	Ser	
305					310					315					320	
tac	tct	gga	ctg	cca	tcc	cat	cca	tcc	tac	cca	tta	gcg	aaa	aaa	tac	1008
Tyr	Ser	Gly	Leu	Pro	Ser	His	Pro	Ser	Tyr	Pro	Leu	Ala	Lys	Lys	Tyr	
				325					330					335		
tta	cct	aaa	ggc	caa	ggg	gct	atc	tta	acg	ttc	gag	gta	aag	ggc	ggc	1056
Leu	Pro	Lys	Gly	Gln	Gly	Ala	Ile	Leu	Thr	Phe	Glu	Val	Lys	Gly	Gly	
			340					345					350			
gtt	gaa	gca	gga	aag	aaa	ctc	att	cat	tcg	gtc	cag	cta	ttc	tcc	cac	1104
Val	Glu	Ala	Gly	Lys	Lys	Leu	Ile	His	Ser	Val	Gln	Leu	Phe	Ser	His	
		355				360					365					
ctt	gcc	aac	gta	ggt	gat	tca	aaa	tcg	ttg	atc	atc	cat	cct	gca	agc	1152
Leu	Ala	Asn	Val	Gly	Asp	Ser	Lys	Ser	Leu	Ile	Ile	His	Pro	Ala	Ser	
		370				375					380					
acg	acc	cac	caa	cag	ctc	tcg	gaa	gca	gaa	cag	cga	gac	gca	gga	gtg	1200
Thr	Thr	His	Gln	Gln	Leu	Ser	Glu	Ala	Glu	Gln	Arg	Asp	Ala	Gly	Val	
					390					395					400	
aca	cct	ggg	atg	atc	aga	ctt	tcg	gta	gga	acc	gaa	tcg	att	cat	gat	1248
Thr	Pro	Gly	Met	Ile	Arg	Leu	Ser	Val	Gly	Thr	Glu	Ser	Ile	His	Asp	
				405					410					415		
att	atc	acc	gat	ctc	aaa	cag	gcg	att	gag	gcg	agt	caa	gcg	taa		1293
Ile	Ile	Thr	Asp	Leu	Lys	Gln	Ala	Ile	Glu	Ala	Ser	Gln	Ala			
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<210> 8

<211> 430

<212> PRT

<213> Bacillus halodurans

<400> 8

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			20					25					30		
Gln	Thr	Thr	Ser	Tyr	Gly	Phe	Lys	Asp	Thr	Asp	His	Ala	Ala	Asn	Leu
			35				40					45			
Phe	Ser	Leu	Ser	Glu	Phe	Gly	Asn	Ile	Tyr	Thr	Arg	Leu	Met	Asn	Pro
	50					55					60				
Thr	Thr	Asp	Val	Phe	Glu	Lys	Arg	Val	Ala	Ala	Leu	Glu	Gly	Gly	Ala
65					70				75						80
Ala	Ala	Leu	Ala	Thr	Ala	Ser	Gly	Gln	Ala	Ala	Ile	Thr	Tyr	Ser	Ile
				85				90						95	
Leu	Asn	Ile	Ala	Glu	Ala	Gly	Asp	Glu	Ile	Val	Ser	Ala	Ser	Ser	Leu
			100					105					110		
Tyr	Gly	Gly	Thr	Tyr	Asn	Leu	Phe	Ser	Ile	Thr	Leu	Pro	Lys	Leu	Gly
		115					120					125			
Val	Asn	Val	Arg	Phe	Val	Asp	Pro	Ser	Asp	Pro	Glu	Asn	Phe	Lys	Ala
	130					135					140				
Ala	Ile	Thr	Glu	Lys	Thr	Lys	Ala	Ile	Phe	Ala	Glu	Ser	Ile	Gly	Asn
145					150					155					160
Pro	Lys	Gly	Asp	Val	Leu	Asp	Ile	Glu	Ala	Val	Ala	Lys	Val	Ala	His
				165					170					175	
Asp	His	His	Leu	Pro	Leu	Ile	Val	Asp	Asn	Thr	Phe	Pro	Ser	Pro	Tyr
			180					185					190		
Leu	Leu	Gln	Pro	Ile	Lys	His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Ala
		195					200					205			
Thr	Lys	Phe	Ile	Gly	Gly	His	Gly	Thr	Ser	Ile	Gly	Gly	Ile	Ile	Val
	210					215					220				
Asp	Gly	Gly	Thr	Phe	Asp	Trp	Ala	Lys	Thr	Asp	Arg	Tyr	Pro	Gly	Leu
225					230					235					240
Thr	Thr	Pro	Asp	Pro	Ser	Tyr	His	Gly	Val	Val	Tyr	Thr	Asp	Ala	Val
				245					250					255	

Gly Pro Ile Ala Tyr Ile Ile Lys Ala Arg Val Gln Leu Leu Arg Asp
 260 265 270

Met Gly Ala Ala Ile Ser Pro Phe Asn Ser Phe Leu Leu Leu Gln Gly
 275 280 285

Leu Glu Thr Leu His Leu Arg Met Glu Arg His Ser Glu Asn Ala Tyr
 290 295 300

Lys Val Ala Glu Phe Leu Glu Gln His Gln Ala Val Glu Ser Val Ser
 305 310 315 320

Tyr Ser Gly Leu Pro Ser His Pro Ser Tyr Pro Leu Ala Lys Lys Tyr
 325 330 335

Leu Pro Lys Gly Gln Gly Ala Ile Leu Thr Phe Glu Val Lys Gly Gly
 340 345 350

Val Glu Ala Gly Lys Lys Leu Ile His Ser Val Gln Leu Phe Ser His
 355 360 365

Leu Ala Asn Val Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser
 370 375 380

Thr Thr His Gln Gln Leu Ser Glu Ala Glu Gln Arg Asp Ala Gly Val
 385 390 395 400

Thr Pro Gly Met Ile Arg Leu Ser Val Gly Thr Glu Ser Ile His Asp
 405 410 415

Ile Ile Thr Asp Leu Lys Gln Ala Ile Glu Ala Ser Gln Ala
 420 425 430

<210> 9

<211> 1203

<212> DNA

<213> Bacillus stearothermophilus

<220>

<221> CDS

<222> (1)..(1203)

<223>

<400> 9

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 Met Ser Tyr Val Phe Arg Asp Ser Glu His Ala Ala Asn Leu Phe Gly

48

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gac gtg ttc gaa aag cgg atc gcg gcg ctt gaa ggc ggc att ggg gcg Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu Gly Gly Ile Gly Ala 35 40 45				144
ctc gcg ctg tca tcg ggg cag gcg gcg gtg ttt tat tcg atc atc aac Leu Ala Leu Ser Ser Gly Gln Ala Ala Val Phe Tyr Ser Ile Ile Asn 50 55 60				192
atc gcc tcg gcg ggc gat gaa atc gtc tcg tct tcg tcc att tac ggc Ile Ala Ser Ala Gly Asp Glu Ile Val Ser Ser Ser Ser Ile Tyr Gly 65 70 75 80				240
gga acg tac aac ttg ttc gcc cat acg ctg cgc aag ttc ggc att acg Gly Thr Tyr Asn Leu Phe Ala His Thr Leu Arg Lys Phe Gly Ile Thr 85 90 95				288
gtg aag ttt gtc gat ccg tcc gac ccc gaa aac ttt gag cgg gcg atc Val Lys Phe Val Asp Pro Ser Asp Pro Glu Asn Phe Glu Arg Ala Ile 100 105 110				336
acc gac aaa acg aaa gcc ttg ttt gcg gaa acg atc ggc aac ccg aaa Thr Asp Lys Thr Lys Ala Leu Phe Ala Glu Thr Ile Gly Asn Pro Lys 115 120 125				384
aac gat gtg ttg gac att gaa gcg gtg gcc gac atc gcc cat cgc cat Asn Asp Val Leu Asp Ile Glu Ala Val Ala Asp Ile Ala His Arg His 130 135 140				432
gcc att ccg ctc att gtc gac aac acg gtg gcc agt cca tac tta ttg Ala Ile Pro Leu Ile Val Asp Asn Thr Val Ala Ser Pro Tyr Leu Leu 145 150 155 160				480
cgg ccg att gaa ttc ggc gcc gat atc gtc gtc cac tca gcg acg aag Arg Pro Ile Glu Phe Gly Ala Asp Ile Val Val His Ser Ala Thr Lys 165 170 175				528
ttc atc ggc ggg cac ggc aat tcg atc ggc ggt gtg att gtg gac agc Phe Ile Gly Gly His Gly Asn Ser Ile Gly Gly Val Ile Val Asp Ser 180 185 190				576
ggc aag ttt gac tgg aaa ggg agc ggc aag ttt ccg gag ttc acc gag Gly Lys Phe Asp Trp Lys Gly Ser Gly Lys Phe Pro Glu Phe Thr Glu 195 200 205				624
cca gac cca agc tac cac ggt ttg gtg tat gtg gac gcc gtc ggc gaa Pro Asp Pro Ser Tyr His Gly Leu Val Tyr Val Asp Ala Val Gly Glu 210 215 220				672
gcg gcg tac atc acg aaa gcg cgc atc cag ctc ttg cgc gat ttg gga Ala Ala Tyr Ile Thr Lys Ala Arg Ile Gln Leu Leu Arg Asp Leu Gly 225 230 235 240				720
gcg gcg ttg tcg ccg ttt aat gcg ttt ttg ctt ttg caa ggg ttg gag Ala Ala Leu Ser Pro Phe Asn Ala Phe Leu Leu Leu Gln Gly Leu Glu 245 250 255				768
acg ctc cat ttg cgg atg cag cgc cat agc gaa aac gcc ctt gcc gtc Thr Leu His Leu Arg Met Gln Arg His Ser Glu Asn Ala Leu Ala Val 260 265 270				816
gcc aag ttt tta gaa gag gaa gaa gcg gtc gaa tcg gtc aat tac cca				864

Ala	Lys	Phe	Leu	Glu	Glu	Glu	Glu	Ala	Val	Glu	Ser	Val	Asn	Tyr	Pro		
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Gly	Leu	Pro	Ser	His	Pro	Ser	His	Glu	Leu	Ala	Lys	Lys	Tyr	Leu	Pro		
	290					295					300						
aac	ggg	caa	gga	gcg	atc	gtc	acg	ttt	gaa	atc	aaa	ggc	ggc	gtc	gaa		960
Asn	Gly	Gln	Gly	Ala	Ile	Val	Thr	Phe	Glu	Ile	Lys	Gly	Gly	Val	Glu		
	305				310					315					320		
gcc	ggc	aaa	aaa	ctg	atc	gac	tcg	gtc	aaa	ctg	ttc	tct	cat	ttg	gcc		1008
Ala	Gly	Lys	Lys	Leu	Ile	Asp	Ser	Val	Lys	Leu	Phe	Ser	His	Leu	Ala		
				325					330					335			
aac	atc	ggc	gat	tcg	aaa	tcg	ctc	atc	atc	cac	ccg	gcc	agc	aca	acg		1056
Asn	Ile	Gly	Asp	Ser	Lys	Ser	Leu	Ile	Ile	His	Pro	Ala	Ser	Thr	Thr		
			340					345					350				
cac	gag	cag	ctg	agc	cca	gat	gaa	cag	ctg	tcc	gcc	ggc	gtc	acc	cca		1104
His	Glu	Gln	Leu	Ser	Pro	Asp	Glu	Gln	Leu	Ser	Ala	Gly	Val	Thr	Pro		
		355					360					365					
ggc	ctt	gtg	cgt	ctg	tcc	gtc	ggc	aca	gaa	gcg	atc	gac	gac	att	ttg		1152
Gly	Leu	Val	Arg	Leu	Ser	Val	Gly	Thr	Glu	Ala	Ile	Asp	Asp	Ile	Leu		
	370					375					380						
gac	gac	ttg	cgc	caa	gcc	att	cgc	caa	agc	cag	acg	gtg	ggg	gtg	aag		1200
Asp	Asp	Leu	Arg	Gln	Ala	Ile	Arg	Gln	Ser	Gln	Thr	Val	Gly	Val	Lys		
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<210> 10

<211> 400

<212> PRT

<213> Bacillus stearothermophilus

<400> 10

Met	Ser	Tyr	Val	Phe	Arg	Asp	Ser	Glu	His	Ala	Ala	Asn	Leu	Phe	Gly		
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Leu	Lys	Glu	Glu	Gly	Phe	Ile	Tyr	Thr	Arg	Ile	Met	Asn	Pro	Thr	Asn		
		20						25					30				
Asp	Val	Phe	Glu	Lys	Arg	Ile	Ala	Ala	Leu	Glu	Gly	Gly	Ile	Gly	Ala		
		35					40					45					
Leu	Ala	Leu	Ser	Ser	Gly	Gln	Ala	Ala	Val	Phe	Tyr	Ser	Ile	Ile	Asn		
	50					55					60						
Ile	Ala	Ser	Ala	Gly	Asp	Glu	Ile	Val	Ser	Ser	Ser	Ser	Ile	Tyr	Gly		
	65				70					75					80		
Gly	Thr	Tyr	Asn	Leu	Phe	Ala	His	Thr	Leu	Arg	Lys	Phe	Gly	Ile	Thr		

85					90					95					
Val	Lys	Phe	Val	Asp	Pro	Ser	Asp	Pro	Glu	Asn	Phe	Glu	Arg	Ala	Ile
			100					105					110		
Thr	Asp	Lys	Thr	Lys	Ala	Leu	Phe	Ala	Glu	Thr	Ile	Gly	Asn	Pro	Lys
		115					120					125			
Asn	Asp	Val	Leu	Asp	Ile	Glu	Ala	Val	Ala	Asp	Ile	Ala	His	Arg	His
	130					135					140				
Ala	Ile	Pro	Leu	Ile	Val	Asp	Asn	Thr	Val	Ala	Ser	Pro	Tyr	Leu	Leu
145					150					155					160
Arg	Pro	Ile	Glu	Phe	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Ala	Thr	Lys
				165					170					175	
Phe	Ile	Gly	Gly	His	Gly	Asn	Ser	Ile	Gly	Gly	Val	Ile	Val	Asp	Ser
			180					185					190		
Gly	Lys	Phe	Asp	Trp	Lys	Gly	Ser	Gly	Lys	Phe	Pro	Glu	Phe	Thr	Glu
		195					200					205			
Pro	Asp	Pro	Ser	Tyr	His	Gly	Leu	Val	Tyr	Val	Asp	Ala	Val	Gly	Glu
	210					215					220				
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225					230					235					240
Ala	Ala	Leu	Ser	Pro	Phe	Asn	Ala	Phe	Leu	Leu	Leu	Gln	Gly	Leu	Glu
				245					250					255	
Thr	Leu	His	Leu	Arg	Met	Gln	Arg	His	Ser	Glu	Asn	Ala	Leu	Ala	Val
			260					265					270		
Ala	Lys	Phe	Leu	Glu	Glu	Glu	Glu	Ala	Val	Glu	Ser	Val	Asn	Tyr	Pro
		275					280					285			
Gly	Leu	Pro	Ser	His	Pro	Ser	His	Glu	Leu	Ala	Lys	Lys	Tyr	Leu	Pro
	290					295					300				
Asn	Gly	Gln	Gly	Ala	Ile	Val	Thr	Phe	Glu	Ile	Lys	Gly	Gly	Val	Glu
305					310					315					320
Ala	Gly	Lys	Lys	Leu	Ile	Asp	Ser	Val	Lys	Leu	Phe	Ser	His	Leu	Ala
				325					330					335	
Asn	Ile	Gly	Asp	Ser	Lys	Ser	Leu	Ile	Ile	His	Pro	Ala	Ser	Thr	Thr
			340					345					350		

His Glu Gln Leu Ser Pro Asp Glu Gln Leu Ser Ala Gly Val Thr Pro
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Gly Leu Val Arg Leu Ser Val Gly Thr Glu Ala Ile Asp Asp Ile Leu
 370 375 380

Asp Asp Leu Arg Gln Ala Ile Arg Gln Ser Gln Thr Val Gly Val Lys
 385 390 395 400

<210> 11

<211> 1290

<212> DNA

<213> Chlorobium tepidum

<220>

<221> CDS

<222> (1)..(1290)

<223>

<400> 11

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ggg cag gag cct gat ccg gtg acc gga tcg cgc gcc gtg ccc att tac	96
Gly Gln Glu Pro Asp Pro Val Thr Gly Ser Arg Ala Val Pro Ile Tyr	
20 25 30	
cag acc acc tcc tac gtg ttc gag aac gcc gag cac ggc gct gac ctg	144
Gln Thr Thr Ser Tyr Val Phe Glu Asn Ala Glu His Gly Ala Asp Leu	
35 40 45	
ttc gcg ctt cgc aag gcg ggc aat atc tac acg cgc ctg atg aac ccg	192
Phe Ala Leu Arg Lys Ala Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro	
50 55 60	
acc acc gac gtg ctc gaa aag cgc atg gcg gcg ctc gaa ggg ggc aag	240
Thr Thr Asp Val Leu Glu Lys Arg Met Ala Ala Leu Glu Gly Gly Lys	
65 70 75 80	
gcg gcc ctc ggc gtg gcg agc ggc cac tcg gcg cag ttc atc gct att	288
Ala Ala Leu Gly Val Ala Ser Gly His Ser Ala Gln Phe Ile Ala Ile	
85 90 95	
gcc acc atc tgc cag gct gga gac aac att gtg tca tcg agc tat ctc	336
Ala Thr Ile Cys Gln Ala Gly Asp Asn Ile Val Ser Ser Ser Tyr Leu	
100 105 110	
tac ggc ggc acc tac aac cag ttc aag gtc gcc ttc aag cgc ctc ggc	384
Tyr Gly Gly Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly	
115 120 125	
atc gag gtg agg ttc gtg gat ggc aac gat cag gag gcg ttc cgc aag	432

Ile	Glu	Val	Arg	Phe	Val	Asp	Gly	Asn	Asp	Gln	Glu	Ala	Phe	Arg	Lys	
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Ala	Ile	Asp	Glu	Asn	Thr	Lys	Ala	Leu	Tyr	Met	Glu	Ser	Ser	Gly	Asn	
145					150					155					160	
ccg	gcg	ttc	cat	gtg	ccc	gat	ttc	gac	gct	atc	gcg	aag	att	gcc	cgt	528
Pro	Ala	Phe	His	Val	Pro	Asp	Phe	Asp	Ala	Ile	Ala	Lys	Ile	Ala	Arg	
				165					170					175		
gag	aac	ggc	att	ccg	ctg	atc	gtc	gat	aac	acc	ttt	ggc	tgc	gcg	ggc	576
Glu	Asn	Gly	Ile	Pro	Leu	Ile	Val	Asp	Asn	Thr	Phe	Gly	Cys	Ala	Gly	
			180					185					190			
tat	ctc	tgc	cgt	ccc	att	gat	cac	ggc	gcg	tcg	atc	gtg	gtc	gag	tcg	624
Tyr	Leu	Cys	Arg	Pro	Ile	Asp	His	Gly	Ala	Ser	Ile	Val	Val	Glu	Ser	
		195					200					205				
gcc	acc	aag	tgg	atc	ggc	ggg	cac	ggc	acc	tcg	atg	ggc	ggc	atc	atc	672
Ala	Thr	Lys	Trp	Ile	Gly	Gly	His	Gly	Thr	Ser	Met	Gly	Gly	Ile	Ile	
	210					215					220					
gtc	gat	gcc	gga	acg	ttc	gac	tgg	ggc	aac	ggc	aag	ttt	ccg	ctc	ttt	720
Val	Asp	Ala	Gly	Thr	Phe	Asp	Trp	Gly	Asn	Gly	Lys	Phe	Pro	Leu	Phe	
225					230					235					240	
acc	gag	cca	tcg	gaa	ggc	tat	cac	ggc	ctg	aaa	ttc	tac	gaa	gcg	gtc	768
Thr	Glu	Pro	Ser	Glu	Gly	Tyr	His	Gly	Leu	Lys	Phe	Tyr	Glu	Ala	Val	
				245					250					255		
ggc	gag	ctg	gcc	ttt	atc	atc	cgg	gcg	cgg	gtc	gag	gga	ctg	cgg	gat	816
Gly	Glu	Leu	Ala	Phe	Ile	Ile	Arg	Ala	Arg	Val	Glu	Gly	Leu	Arg	Asp	
			260					265					270			
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Phe	Gly	Pro	Ala	Ile	Ser	Pro	Phe	Asn	Ser	Phe	Met	Leu	Leu	Gln	Gly	
		275					280					285				
ctt	gaa	acg	ctc	tcg	ctt	cgc	gtg	cag	cgc	cac	ctc	gac	aac	acg	ctt	912
Leu	Glu	Thr	Leu	Ser	Leu	Arg	Val	Gln	Arg	His	Leu	Asp	Asn	Thr	Leu	
	290					295					300					
gaa	ctg	gcc	cgc	tgg	ctc	gaa	agg	cac	gat	gcg	gtt	gcg	tgg	gtg	aac	960
Glu	Leu	Ala	Arg	Trp	Leu	Glu	Arg	His	Asp	Ala	Val	Ala	Trp	Val	Asn	
305					310					315					320	
tat	cca	ggc	ctc	gaa	agc	cat	ccg	aca	cac	gcc	ctg	gca	aaa	aaa	tat	1008
Tyr	Pro	Gly	Leu	Glu	Ser	His	Pro	Thr	His	Ala	Leu	Ala	Lys	Lys	Tyr	
				325					330					335		
ctc	acg	cat	ggc	ttc	ggc	tgc	gtg	ctg	act	ttc	ggc	gtg	aag	ggt	ggt	1056
Leu	Thr	His	Gly	Phe	Gly	Cys	Val	Leu	Thr	Phe	Gly	Val	Lys	Gly	Gly	
			340					345					350			
tat	gaa	aac	gcg	gtg	aag	ttc	atc	gac	agc	gtg	aag	ctg	gcg	agc	cac	1104
Tyr	Glu	Asn	Ala	Val	Lys	Phe	Ile	Asp	Ser	Val	Lys	Leu	Ala	Ser	His	
		355					360					365				
ctg	gcc	aac	gtg	ggt	gat	gca	aaa	acg	ctc	gtc	att	cat	ccg	gca	tcg	1152
Leu	Ala	Asn	Val	Gly	Asp	Ala	Lys	Thr	Leu	Val	Ile	His	Pro	Ala	Ser	
	370					375					380					
acg	acg	cac	cag	cag	ctc	agc	gcc	gag	gaa	cag	gta	tcg	gcg	ggc	gtc	1200
Thr	Thr	His	Gln	Gln	Leu	Ser	Ala	Glu	Glu	Gln	Val	Ser	Ala	Gly	Val	
385					390					395					400	

acc gcc gat atg gtg cgc gtg tcg gtt ggt atc gag cat atc gat gac 1248
 Thr Ala Asp Met Val Arg Val Ser Val Gly Ile Glu His Ile Asp Asp
 405 410 415

atc aag gct gat ttc agc cag gct ttc gag aat tta gca tga 1290
 Ile Lys Ala Asp Phe Ser Gln Ala Phe Glu Asn Leu Ala
 420 425

<210> 12

<211> 429

<212> PRT

<213> Chlorobium tepidum

<400> 12

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Gly Gln Glu Pro Asp Pro Val Thr Gly Ser Arg Ala Val Pro Ile Tyr
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Gln Thr Thr Ser Tyr Val Phe Glu Asn Ala Glu His Gly Ala Asp Leu
 35 40 45

Phe Ala Leu Arg Lys Ala Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro
 50 55 60

Thr Thr Asp Val Leu Glu Lys Arg Met Ala Ala Leu Glu Gly Gly Lys
 65 70 75 80

Ala Ala Leu Gly Val Ala Ser Gly His Ser Ala Gln Phe Ile Ala Ile
 85 90 95

Ala Thr Ile Cys Gln Ala Gly Asp Asn Ile Val Ser Ser Ser Tyr Leu
 100 105 110

Tyr Gly Gly Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly
 115 120 125

Ile Glu Val Arg Phe Val Asp Gly Asn Asp Gln Glu Ala Phe Arg Lys
 130 135 140

Ala Ile Asp Glu Asn Thr Lys Ala Leu Tyr Met Glu Ser Ser Gly Asn
 145 150 155 160

Pro Ala Phe His Val Pro Asp Phe Asp Ala Ile Ala Lys Ile Ala Arg
 165 170 175

Glu Asn Gly Ile Pro Leu Ile Val Asp Asn Thr Phe Gly Cys Ala Gly
 180 185 190

Tyr Leu Cys Arg Pro Ile Asp His Gly Ala Ser Ile Val Val Glu Ser
 195 200 205

Ala Thr Lys Trp Ile Gly Gly His Gly Thr Ser Met Gly Gly Ile Ile
 210 215 220

Val Asp Ala Gly Thr Phe Asp Trp Gly Asn Gly Lys Phe Pro Leu Phe
 225 230 235 240

Thr Glu Pro Ser Glu Gly Tyr His Gly Leu Lys Phe Tyr Glu Ala Val
 245 250 255

Gly Glu Leu Ala Phe Ile Ile Arg Ala Arg Val Glu Gly Leu Arg Asp
 260 265 270

Phe Gly Pro Ala Ile Ser Pro Phe Asn Ser Phe Met Leu Leu Gln Gly
 275 280 285

Leu Glu Thr Leu Ser Leu Arg Val Gln Arg His Leu Asp Asn Thr Leu
 290 295 300

Glu Leu Ala Arg Trp Leu Glu Arg His Asp Ala Val Ala Trp Val Asn
 305 310 315 320

Tyr Pro Gly Leu Glu Ser His Pro Thr His Ala Leu Ala Lys Lys Tyr
 325 330 335

Leu Thr His Gly Phe Gly Cys Val Leu Thr Phe Gly Val Lys Gly Gly
 340 345 350

Tyr Glu Asn Ala Val Lys Phe Ile Asp Ser Val Lys Leu Ala Ser His
 355 360 365

Leu Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser
 370 375 380

Thr Thr His Gln Gln Leu Ser Ala Glu Glu Gln Val Ser Ala Gly Val
 385 390 395 400

Thr Ala Asp Met Val Arg Val Ser Val Gly Ile Glu His Ile Asp Asp
 405 410 415

Ile Lys Ala Asp Phe Ser Gln Ala Phe Glu Asn Leu Ala
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<210> 13

<211> 1281

<212> DNA

<213> *Lactococcus lactis*

<220>

<221> CDS

<222> (1)..(1281)

<223>

<400> 13

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caa gtc cct gat cct gtc acg ggt tca cgc gcc gtt ccg ctc tat caa	96
Gln Val Pro Asp Pro Val Thr Gly Ser Arg Ala Val Pro Leu Tyr Gln	
20 25 30	
aca act tct ttc gtt ttt aac aat tca gac cat gcc gaa gct cgt ttt	144
Thr Thr Ser Phe Val Phe Asn Asn Ser Asp His Ala Glu Ala Arg Phe	
35 40 45	
gct tta caa gat cct gga gct att tat tca cgt tta gga aat cca acc	192
Ala Leu Gln Asp Pro Gly Ala Ile Tyr Ser Arg Leu Gly Asn Pro Thr	
50 55 60	
aac gat gtt ttt gaa gca cgc atc gca gct ctt gaa ggt gga agt gca	240
Asn Asp Val Phe Glu Ala Arg Ile Ala Ala Leu Glu Gly Gly Ser Ala	
65 70 75 80	
gcc ctt ggt gtt ggt tct ggc tca gcc gct att acc tat gcc atc ttg	288
Ala Leu Gly Val Ser Gly Ser Ala Ala Ile Thr Tyr Ala Ile Leu	
85 90 95	
aat atc gct aca gtc ggt gat aat att gtt tcc gca agt acc ctt tat	336
Asn Ile Ala Thr Val Gly Asp Asn Ile Val Ser Ala Ser Thr Leu Tyr	
100 105 110	
ggt gga acc tat cac ctt ttt tct ggg act tta cca aaa tat gga att	384
Gly Gly Thr Tyr His Leu Phe Ser Gly Thr Leu Pro Lys Tyr Gly Ile	
115 120 125	
aca act aaa ttt gtc aat cca gat gac ccg aag aat ttt gaa gag gcg	432
Thr Thr Lys Phe Val Asn Pro Asp Asp Pro Lys Asn Phe Glu Glu Ala	
130 135 140	
att gat gaa aaa acc aaa gct att tat tat gaa act ttg ggc aat ccg	480
Ile Asp Glu Lys Thr Lys Ala Ile Tyr Tyr Glu Thr Leu Gly Asn Pro	
145 150 155 160	
gga aat aat gtg att gat tat gat gcc att ggt caa att gct aaa aaa	528
Gly Asn Asn Val Ile Asp Tyr Asp Ala Ile Gly Gln Ile Ala Lys Lys	
165 170 175	
cat gga att ccc gtt att gtt gat gca acg ttt act acc cct gtg acc	576
His Gly Ile Pro Val Ile Val Asp Ala Thr Phe Thr Thr Pro Val Thr	
180 185 190	
ttt aaa cca ttt gaa cat ggt gct aat gta att gtt cat tca gca acg	624

Phe	Lys	Pro	Phe	Glu	His	Gly	Ala	Asn	Val	Ile	Val	His	Ser	Ala	Thr	
		195					200					205				
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Lys	Phe	Ile	Gly	Gly	His	Gly	Thr	Ser	Ile	Gly	Gly	Val	Ile	Val	Asp	
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ggc	gga	aac	ttt	gat	tgg	gca	aat	ggt	aat	ttt	cct	gat	ttt	aca	caa	720
Gly	Gly	Asn	Phe	Asp	Trp	Ala	Asn	Gly	Asn	Phe	Pro	Asp	Phe	Thr	Gln	
225					230					235					240	
gct	gat	gaa	agc	tac	aat	ggg	att	aaa	ttt	gcc	gaa	ttg	ggt	gaa	att	768
Ala	Asp	Glu	Ser	Tyr	Asn	Gly	Ile	Lys	Phe	Ala	Glu	Leu	Gly	Glu	Ile	
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gct	ttt	gtg	act	cgg	gtt	aga	gct	att	tta	tta	cgt	gat	acg	ggt	gcg	816
Ala	Phe	Val	Thr	Arg	Val	Arg	Ala	Ile	Leu	Leu	Arg	Asp	Thr	Gly	Ala	
			260					265					270			
gct	tta	tca	cct	ttt	cat	tct	tgg	ctt	ttc	tta	cag	ggg	cta	gaa	aca	864
Ala	Leu	Ser	Pro	Phe	His	Ser	Trp	Leu	Phe	Leu	Gln	Gly	Leu	Glu	Thr	
		275					280					285				
ctc	tca	ctc	cgg	gta	gaa	cgt	cac	atc	tcc	aat	act	aaa	aag	att	gta	912
Leu	Ser	Leu	Arg	Val	Glu	Arg	His	Ile	Ser	Asn	Thr	Lys	Lys	Ile	Val	
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gaa	ttt	tta	gac	aat	cat	cct	aag	gtg	gaa	ctt	gtt	aac	cat	cct	ctg	960
Glu	Phe	Leu	Asp	Asn	His	Pro	Lys	Val	Glu	Leu	Val	Asn	His	Pro	Leu	
305					310					315					320	
ctt	gaa	agt	aat	tcc	tat	cat	gcg	ctc	tat	cag	aaa	tat	tat	cca	aaa	1008
Leu	Glu	Ser	Asn	Ser	Tyr	His	Ala	Leu	Tyr	Gln	Lys	Tyr	Tyr	Pro	Lys	
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gat	gct	gga	tct	atc	ttt	acc	ttt	gaa	ctc	aaa	gac	aaa	gat	gag	aaa	1056
Asp	Ala	Gly	Ser	Ile	Phe	Thr	Phe	Glu	Leu	Lys	Asp	Lys	Asp	Glu	Lys	
			340					345					350			
aaa	gcg	cgt	gat	ttg	att	gat	cat	ctt	gaa	att	ttc	tca	ctt	cta	gcc	1104
Lys	Ala	Arg	Asp	Leu	Ile	Asp	His	Leu	Glu	Ile	Phe	Ser	Leu	Leu	Ala	
		355					360					365				
aac	gtt	gga	gat	acc	aaa	tca	ttg	gcc	att	cat	cct	gct	tcg	acc	act	1152
Asn	Val	Gly	Asp	Thr	Lys	Ser	Leu	Ala	Ile	His	Pro	Ala	Ser	Thr	Thr	
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cac	cag	cag	ctg	aat	gcc	gaa	gaa	ctt	gct	agt	gca	ggg	att	tcc	aaa	1200
His	Gln	Gln	Leu	Asn	Ala	Glu	Glu	Leu	Ala	Ser	Ala	Gly	Ile	Ser	Lys	
385					390					395					400	
gga	acc	att	cga	tta	tcg	gtt	ggt	att	gaa	gat	gta	act	gac	ttg	att	1248
Gly	Thr	Ile	Arg	Leu	Ser	Val	Gly	Ile	Glu	Asp	Val	Thr	Asp	Leu	Ile	
				405					410					415		
gct	gat	tta	gag	caa	gca	tta	gaa	aaa	ata	taa						1281
Ala	Asp	Leu	Glu	Gln	Ala	Leu	Glu	Lys	Ile							
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<210> 14

<211> 426

<212> PRT

<213> *Lactococcus lactis*

<400> 14

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Thr Thr Ser Phe Val Phe Asn Asn Ser Asp His Ala Glu Ala Arg Phe
          35          40          45

Ala Leu Gln Asp Pro Gly Ala Ile Tyr Ser Arg Leu Gly Asn Pro Thr
50          55          60

Asn Asp Val Phe Glu Ala Arg Ile Ala Ala Leu Glu Gly Gly Ser Ala
65          70          75          80

Ala Leu Gly Val Gly Ser Gly Ser Ala Ala Ile Thr Tyr Ala Ile Leu
          85          90          95

Asn Ile Ala Thr Val Gly Asp Asn Ile Val Ser Ala Ser Thr Leu Tyr
          100          105          110

Gly Gly Thr Tyr His Leu Phe Ser Gly Thr Leu Pro Lys Tyr Gly Ile
          115          120          125

Thr Thr Lys Phe Val Asn Pro Asp Asp Pro Lys Asn Phe Glu Glu Ala
          130          135          140

Ile Asp Glu Lys Thr Lys Ala Ile Tyr Tyr Glu Thr Leu Gly Asn Pro
145          150          155          160

Gly Asn Asn Val Ile Asp Tyr Asp Ala Ile Gly Gln Ile Ala Lys Lys
          165          170          175

His Gly Ile Pro Val Ile Val Asp Ala Thr Phe Thr Thr Pro Val Thr
          180          185          190

Phe Lys Pro Phe Glu His Gly Ala Asn Val Ile Val His Ser Ala Thr
          195          200          205

Lys Phe Ile Gly Gly His Gly Thr Ser Ile Gly Gly Val Ile Val Asp
210          215          220

Gly Gly Asn Phe Asp Trp Ala Asn Gly Asn Phe Pro Asp Phe Thr Gln
225          230          235          240

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Ala Asp Glu Ser Tyr Asn Gly Ile Lys Phe Ala Glu Leu Gly Glu Ile
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Ala Phe Val Thr Arg Val Arg Ala Ile Leu Leu Arg Asp Thr Gly Ala
 260 265 270

Ala Leu Ser Pro Phe His Ser Trp Leu Phe Leu Gln Gly Leu Glu Thr
 275 280 285

Leu Ser Leu Arg Val Glu Arg His Ile Ser Asn Thr Lys Lys Ile Val
 290 295 300

Glu Phe Leu Asp Asn His Pro Lys Val Glu Leu Val Asn His Pro Leu
 305 310 315 320

Leu Glu Ser Asn Ser Tyr His Ala Leu Tyr Gln Lys Tyr Tyr Pro Lys
 325 330 335

Asp Ala Gly Ser Ile Phe Thr Phe Glu Leu Lys Asp Lys Asp Glu Lys
 340 345 350

Lys Ala Arg Asp Leu Ile Asp His Leu Glu Ile Phe Ser Leu Leu Ala
 355 360 365

Asn Val Gly Asp Thr Lys Ser Leu Ala Ile His Pro Ala Ser Thr Thr
 370 375 380

His Gln Gln Leu Asn Ala Glu Glu Leu Ala Ser Ala Gly Ile Ser Lys
 385 390 395 400

Gly Thr Ile Arg Leu Ser Val Gly Ile Glu Asp Val Thr Asp Leu Ile
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Ala Asp Leu Glu Gln Ala Leu Glu Lys Ile
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<210> 15

<211> 1173

<212> DNA

<213> Synechococcus sp.

<220>

<221> CDS

<222> (1)..(1173)

<223>

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gac tcg gcc acc aat gcc aga gcg gtg ccg att tat cag acc agc tcc	96															
Asp Ser Ala Thr Asn Ala Arg Ala Val Pro Ile Tyr Gln Thr Ser Ser																
20 25 30																
tac gtc ttc aac gac gcc gag cac ggc gcc aac ctg ttt gga ctg aag	144															
Tyr Val Phe Asn Asp Ala Glu His Gly Ala Asn Leu Phe Gly Leu Lys																
35 40 45																
gaa ttc ggc aac atc tac acc cgt ctg atg aac ccg acg acg gat gtg	192															
Glu Phe Gly Asn Ile Tyr Thr Arg Leu Met Asn Pro Thr Thr Asp Val																
50 55 60																
ttc gag aag cgg gtg gcg gcc ctg gaa ggg ggt gtg gcc gcg ctg gcc	240															
Phe Glu Lys Arg Val Ala Ala Leu Glu Gly Gly Val Ala Ala Leu Ala																
65 70 75 80																
aca gcc tcc ggt cag tcg gct cag ttc ctg gcg atc acg aat tgc atg	288															
Thr Ala Ser Gly Gln Ser Ala Gln Phe Leu Ala Ile Thr Asn Cys Met																
85 90 95																
cag gca ggg gat aac ttt gtg tcc acg tcg ttc ctt tac ggc ggc acc	336															
Gln Ala Gly Asp Asn Phe Val Ser Thr Ser Phe Leu Tyr Gly Gly Thr																
100 105 110																
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115 120 125																
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130 135 140																
aaa acc aaa ggc ctc tac gtc gaa gcg atg ggc aat cca cgc ttc aac	480															
Lys Thr Lys Gly Leu Tyr Val Glu Ala Met Gly Asn Pro Arg Phe Asn																
145 150 155 160																
atc ccc gat ttc gag ggc ctc tca gcc ctg gct aaa gag cgc ggc atc	528															
Ile Pro Asp Phe Glu Gly Leu Ser Ala Leu Ala Lys Glu Arg Gly Ile																
165 170 175																
cca ttg atc gtg gac aac acc ttg gga gct tgc ggt gcc ctg atg cgt	576															
Pro Leu Ile Val Asp Asn Thr Leu Gly Ala Cys Gly Ala Leu Met Arg																
180 185 190																
ccg atc gat cat ggc gcg gat gtg gtg gtg gaa agc gcc acc aag tgg	624															
Pro Ile Asp His Gly Ala Asp Val Val Val Glu Ser Ala Thr Lys Trp																
195 200 205																
att ggc ggc cat ggc acc agc ctc ggt ggc gtg atc gtt gat gcc ggc	672															
Ile Gly Gly His Gly Thr Ser Leu Gly Gly Val Ile Val Asp Ala Gly																
210 215 220																
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225 230 235 240																
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245 250 255																
gac gtc tgc aaq atg ctg qqa qtq ccq qac aac cqc aac qtc gcc ttt	816															

Asp	Val	Cys	Lys	Met	Leu	Gly	Val	Pro	Asp	Asn	Arg	Asn	Val	Ala	Phe		
			260					265					270				
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Ala	Leu	Arg	Ala	Arg	Val	Glu	Gly	Leu	Arg	Asp	Trp	Gly	Pro	Ala	Val		
			275				280					285					
agt	ccc	ttc	aat	agc	ttc	ctg	ctg	ctg	caa	ggg	cta	gaa	acc	ctc	agc		912
Ser	Pro	Phe	Asn	Ser	Phe	Leu	Leu	Leu	Gln	Gly	Leu	Glu	Thr	Leu	Ser		
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Leu	Arg	Val	Glu	Arg	His	Thr	Glu	Asn	Ala	Met	Ala	Leu	Ala	Thr	Trp		
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cta	gca	acg	cac	ccc	aat	gtg	gag	cat	gtg	agc	tac	cca	ggc	ctg	agc		1008
Leu	Ala	Thr	His	Pro	Asn	Val	Glu	His	Val	Ser	Tyr	Pro	Gly	Leu	Ser		
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agc	gat	ccg	tat	cac	gca	gct	gcc	aag	aaa	tac	ctg	acg	ggc	cgg	ggc		1056
Ser	Asp	Pro	Tyr	His	Ala	Ala	Ala	Lys	Lys	Tyr	Leu	Thr	Gly	Arg	Gly		
			340					345					350				
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Met	Gly	Cys	Met	Leu	Met	Phe	Ser	Leu	Lys	Gly	Gly	Tyr	Asp	Asp	Ala		
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gtc	cgt	ttc	atc	aac	agc	ctt	caa	ctg	gcc	agt	cac	ctc	gcc	aat	gtg		1152
Val	Arg	Phe	Ile	Asn	Ser	Leu	Gln	Leu	Ala	Ser	His	Leu	Ala	Asn	Val		
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<211> 390

<212> PRT

<213> Synechococcus sp.

<400> 16

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Tyr	Val	Phe	Asn	Asp	Ala	Glu	His	Gly	Ala	Asn	Leu	Phe	Gly	Leu	Lys		
		35					40					45					
Glu	Phe	Gly	Asn	Ile	Tyr	Thr	Arg	Leu	Met	Asn	Pro	Thr	Thr	Asp	Val		
		50				55					60						
Phe	Glu	Lys	Arg	Val	Ala	Ala	Leu	Glu	Gly	Gly	Val	Ala	Ala	Leu	Ala		
65					70					75					80		

Thr Ala Ser Gly Gln Ser Ala Gln Phe Leu Ala Ile Thr Asn Cys Met
 85 90 95
 Gln Ala Gly Asp Asn Phe Val Ser Thr Ser Phe Leu Tyr Gly Gly Thr
 100 105 110
 Tyr Asn Gln Phe Lys Val Gln Phe Pro Arg Leu Gly Ile Asp Val Arg
 115 120 125
 Phe Ala Asp Gly Asp Asp Val Glu Ser Phe Ala Ala Gln Ile Asp Asp
 130 135 140
 Lys Thr Lys Gly Leu Tyr Val Glu Ala Met Gly Asn Pro Arg Phe Asn
 145 150 155 160
 Ile Pro Asp Phe Glu Gly Leu Ser Ala Leu Ala Lys Glu Arg Gly Ile
 165 170 175
 Pro Leu Ile Val Asp Asn Thr Leu Gly Ala Cys Gly Ala Leu Met Arg
 180 185 190
 Pro Ile Asp His Gly Ala Asp Val Val Val Glu Ser Ala Thr Lys Trp
 195 200 205
 Ile Gly Gly His Gly Thr Ser Leu Gly Gly Val Ile Val Asp Ala Gly
 210 215 220
 Thr Phe Asn Trp Gly Asn Gly Lys Phe Pro Leu Leu Ser Gln Pro Ser
 225 230 235 240
 Ala Ala Tyr His Gly Leu Val His Trp Asp Ala Phe Gly Phe Gly Ser
 245 250 255
 Asp Val Cys Lys Met Leu Gly Val Pro Asp Asn Arg Asn Val Ala Phe
 260 265 270
 Ala Leu Arg Ala Arg Val Glu Gly Leu Arg Asp Trp Gly Pro Ala Val
 275 280 285
 Ser Pro Phe Asn Ser Phe Leu Leu Leu Gln Gly Leu Glu Thr Leu Ser
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 Leu Arg Val Glu Arg His Thr Glu Asn Ala Met Ala Leu Ala Thr Trp
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 Leu Ala Thr His Pro Asn Val Glu His Val Ser Tyr Pro Gly Leu Ser
 325 330 335
 Ser Asp Pro Tyr His Ala Ala Ala Lys Lys Tyr Leu Thr Gly Arg Gly
 340 345 350

Met Gly Cys Met Leu Met Phe Ser Leu Lys Gly Gly Tyr Asp Asp Ala
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Val Arg Phe Ile Asn Ser Leu Gln Leu Ala Ser His Leu Ala Asn Val
 370 375 380

Gly Asp Ala Lys Thr Trp
 385 390

<210> 17

<211> 1314

<212> DNA

<213> *Emericella nidulans*

<220>

<221> CDS

<222> (1)..(1314)

<223>

<400> 17

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ggc	cag	gag	cct	gac	cct	gca	act	aat	tcc	cgc	gct	gtc	cca	atc	tat	96
Gly	Gln	Glu	Pro	Asp	Pro	Ala	Thr	Asn	Ser	Arg	Ala	Val	Pro	Ile	Tyr	
			20					25					30			

gcg	aca	acg	tcc	tac	acc	ttc	aat	gac	tcc	gca	cac	ggc	gcc	agg	ctt	144
Ala	Thr	Thr	Ser	Tyr	Thr	Phe	Asn	Asp	Ser	Ala	His	Gly	Ala	Arg	Leu	
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ttt	ggc	ctc	aaa	gag	ttt	ggc	aat	att	tac	agc	cga	att	atg	aat	ccc	192
Phe	Gly	Leu	Lys	Glu	Phe	Gly	Asn	Ile	Tyr	Ser	Arg	Ile	Met	Asn	Pro	
	50					55					60					

aca	gtc	gat	gtc	ttc	gaa	aaa	cgt	att	gct	gca	ctc	gag	gga	ggt	gtc	240
Thr	Val	Asp	Val	Phe	Glu	Lys	Arg	Ile	Ala	Ala	Leu	Glu	Gly	Gly	Val	
65					70				75						80	

gct	gcg	gtg	gct	gcc	tca	tct	ggc	cag	gca	gcc	cag	ttc	atg	gcc	atc	288
Ala	Ala	Val	Ala	Ala	Ser	Ser	Gly	Gln	Ala	Ala	Gln	Phe	Met	Ala	Ile	
				85				90						95		

tct	gct	cta	gcc	cat	gct	ggt	gac	aat	atc	gtt	tcc	aca	agt	aat	ttg	336
Ser	Ala	Leu	Ala	His	Ala	Gly	Asp	Asn	Ile	Val	Ser	Thr	Ser	Asn	Leu	
			100				105						110			

tat	ggt	ggt	aca	tac	aat	cag	ttt	aag	gtc	ctt	ttc	cca	cga	ctg	gga	384
Tyr	Gly	Gly	Thr	Tyr	Asn	Gln	Phe	Lys	Val	Leu	Phe	Pro	Arg	Leu	Gly	
		115					120					125				

att acc aca aaa ttc gtg cag gga gac aaa gca gag gac att gcc gcc Ile Thr Thr Lys Phe Val Gln Gly Asp Lys Ala Glu Asp Ile Ala Ala 130 135 140	432
gct atc gat gac cgt acc aag gcc gtc tac gtc gag aca ata gga aac Ala Ile Asp Asp Arg Thr Lys Ala Val Tyr Val Glu Thr Ile Gly Asn 145 150 155 160	480
cct cgc tac aat gtg ccc gac ttt gag gtc att gca aaa gta gcc cat Pro Arg Tyr Asn Val Pro Asp Phe Glu Val Ile Ala Lys Val Ala His 165 170 175	528
gag aag gga att ccc ctt gtg gtt gac aac acc ttc ggt gcc gga ggc Glu Lys Gly Ile Pro Leu Val Val Asp Asn Thr Phe Gly Ala Gly Gly 180 185 190	576
tac ttt gtt cga ccc att gaa cat ggc gcc gac att gtc gtg cac agt Tyr Phe Val Arg Pro Ile Glu His Gly Ala Asp Ile Val Val His Ser 195 200 205	624
gca act aaa tgg att gga ggt cat ggc aca acc atc gga ggc gtt gtc Ala Thr Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Val Val 210 215 220	672
gtg gac agc ggc aaa ttc gac tgg ggc aag aac gcc gcg cgg ttt cct Val Asp Ser Gly Lys Phe Asp Trp Gly Lys Asn Ala Ala Arg Phe Pro 225 230 235 240	720
cag ttc acg cag cct tct gaa ggt tac cac ggg ttg aac ttc tgg gag Gln Phe Thr Gln Pro Ser Glu Gly Tyr His Gly Leu Asn Phe Trp Glu 245 250 255	768
acc ttc ggc ccc att gcc ttc gcg att cgt gtc cgg gtc gaa atc ctg Thr Phe Gly Pro Ile Ala Phe Ala Ile Arg Val Arg Val Glu Ile Leu 260 265 270	816
cgc gac ctc ggg tcc gcg ctg aac cct ttc gcc gcg cag cag ctc atc Arg Asp Leu Gly Ser Ala Leu Asn Pro Phe Ala Ala Gln Gln Leu Ile 275 280 285	864
ctg ggt ctg gaa acc cta agc ttg cgc gct gag cgt cat gct tcc aac Leu Gly Leu Glu Thr Leu Ser Leu Arg Ala Glu Arg His Ala Ser Asn 290 295 300	912
gct ctg gcc ctc gcc aac tgg cta aag aag aat gat cac gtc agc tgg Ala Leu Ala Leu Ala Asn Trp Leu Lys Lys Asn Asp His Val Ser Trp 305 310 315 320	960
gtt tct tac gtg ggc cta gaa gag cac tcc agc cac gaa gtt gca aag Val Ser Tyr Val Gly Leu Glu Glu His Ser Ser His Glu Val Ala Lys 325 330 335	1008
aag tac ctc aag cgt ggg ttc ggc ggt gtc cta tcc ttt ggt gtc aag Lys Tyr Leu Lys Arg Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys 340 345 350	1056
ggt gag gca gcc gtc ggt agc cag gtt gtc gac aac ttt aag ctc atc Gly Glu Ala Ala Val Gly Ser Gln Val Val Asp Asn Phe Lys Leu Ile 355 360 365	1104
tcc aat cta gca aat gtt gga gac tcc aag acc ctc gcg att cac ccc Ser Asn Leu Ala Asn Val Gly Asp Ser Lys Thr Leu Ala Ile His Pro 370 375 380	1152
tgg agc acc act cac gag cag ttg acc gac cag gag cga atc gat tct Trp Ser Thr Thr His Glu Gln Leu Thr Asp Gln Glu Arg Ile Asp Ser 385 390 395 400	1200

ggt gtt acg gaa gat gcc atc cgc atc tct gtc ggc act gag cac atc 1248
 Gly Val Thr Glu Asp Ala Ile Arg Ile Ser Val Gly Thr Glu His Ile
 405 410 415

gac gac atc atc gcc gac ttt gaa cag tca ttt gca gcg acc ttc aaa 1296
 Asp Asp Ile Ile Ala Asp Phe Glu Gln Ser Phe Ala Ala Thr Phe Lys
 420 425 430

gtt gtc cgg agt gct tag 1314
 Val Val Arg Ser Ala
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<210> 18

<211> 437

<212> PRT

<213> Emericella nidulans

<400> 18

Met Ser Asp Pro Ser Pro Lys Arg Phe Glu Thr Leu Gln Leu His Ala
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Gly Gln Glu Pro Asp Pro Ala Thr Asn Ser Arg Ala Val Pro Ile Tyr
 20 25 30

Ala Thr Thr Ser Tyr Thr Phe Asn Asp Ser Ala His Gly Ala Arg Leu
 35 40 45

Phe Gly Leu Lys Glu Phe Gly Asn Ile Tyr Ser Arg Ile Met Asn Pro
 50 55 60

Thr Val Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu Gly Gly Val
 65 70 75 80

Ala Ala Val Ala Ala Ser Ser Gly Gln Ala Ala Gln Phe Met Ala Ile
 85 90 95

Ser Ala Leu Ala His Ala Gly Asp Asn Ile Val Ser Thr Ser Asn Leu
 100 105 110

Tyr Gly Gly Thr Tyr Asn Gln Phe Lys Val Leu Phe Pro Arg Leu Gly
 115 120 125

Ile Thr Thr Lys Phe Val Gln Gly Asp Lys Ala Glu Asp Ile Ala Ala
 130 135 140

Ala Ile Asp Asp Arg Thr Lys Ala Val Tyr Val Glu Thr Ile Gly Asn
 145 150 155 160

Pro Arg Tyr Asn Val Pro Asp Phe Glu Val Ile Ala Lys Val Ala His

165								170					175			
Glu	Lys	Gly	Ile 180	Pro	Leu	Val	Val	Asp 185	Asn	Thr	Phe	Gly	Ala 190	Gly	Gly	
Tyr	Phe	Val 195	Arg	Pro	Ile	Glu	His 200	Gly	Ala	Asp	Ile	Val 205	Val	His	Ser	
Ala	Thr 210	Lys	Trp	Ile	Gly	Gly 215	His	Gly	Thr	Thr	Ile 220	Gly	Gly	Val	Val	
Val	Asp	Ser	Gly	Lys	Phe	Asp	Trp	Gly	Lys	Asn	Ala	Ala	Arg	Phe	Pro	
225				230				235				240				
Gln	Phe	Thr	Gln	Pro 245	Ser	Glu	Gly	Tyr	His 250	Gly	Leu	Asn	Phe	Trp 255	Glu	
Thr	Phe	Gly	Pro 260	Ile	Ala	Phe	Ala	Ile 265	Arg	Val	Arg	Val	Glu 270	Ile	Leu	
Arg	Asp	Leu 275	Gly	Ser	Ala	Leu	Asn 280	Pro	Phe	Ala	Ala	Gln 285	Gln	Leu	Ile	
Leu	Gly 290	Leu	Glu	Thr	Leu	Ser 295	Leu	Arg	Ala	Glu	Arg 300	His	Ala	Ser	Asn	
Ala 305	Leu	Ala	Leu	Ala	Asn 310	Trp	Leu	Lys	Lys	Asn 315	Asp	His	Val	Ser	Trp 320	
Val	Ser	Tyr	Val	Gly 325	Leu	Glu	Glu	His	Ser 330	Ser	His	Glu	Val	Ala 335	Lys	
Lys	Tyr	Leu	Lys 340	Arg	Gly	Phe	Gly	Gly 345	Val	Leu	Ser	Phe	Gly 350	Val	Lys	
Gly	Glu	Ala 355	Ala	Val	Gly	Ser	Gln 360	Val	Val	Asp	Asn	Phe 365	Lys	Leu	Ile	
Ser	Asn 370	Leu	Ala	Asn	Val	Gly 375	Asp	Ser	Lys	Thr	Leu 380	Ala	Ile	His	Pro	
Trp 385	Ser	Thr	Thr	His	Glu 390	Gln	Leu	Thr	Asp	Gln 395	Glu	Arg	Ile	Asp	Ser 400	
Gly	Val	Thr	Glu	Asp 405	Ala	Ile	Arg	Ile	Ser 410	Val	Gly	Thr	Glu	His 415	Ile	
Asp	Asp	Ile	Ile 420	Ala	Asp	Phe	Glu	Gln 425	Ser	Phe	Ala	Ala	Thr 430	Phe	Lys	

Val Val Arg Ser Ala
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<210> 19

<211> 1287

<212> DNA

<213> Bacteroides fragilis

<220>

<221> CDS

<222> (1)..(1287)

<223>

<400> 19

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Met Glu Thr Lys Lys Leu His Phe Glu Thr Leu Gln Leu His Val Gly	
1 5 10 15	
cag gag act ccc gac ccg gca acc gat gcg cgt gcc gta cct att tat	96
Gln Glu Thr Pro Asp Pro Ala Thr Asp Ala Arg Ala Val Pro Ile Tyr	
20 25 30	
cag aca act tcc tat gtg ttc cgg gat tcg gcc cat gcc gcc gca cga	144
Gln Thr Thr Ser Tyr Val Phe Arg Asp Ser Ala His Ala Ala Ala Arg	
35 40 45	
ttt gga ttg caa gac cct ggg aat att tat gga cga ctg acc aat tcc	192
Phe Gly Leu Gln Asp Pro Gly Asn Ile Tyr Gly Arg Leu Thr Asn Ser	
50 55 60	
act cag gga gta ttg gag gaa cgc atc gca gca ctt gaa ggg gga gta	240
Thr Gln Gly Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Val	
65 70 75 80	
ggt ggg ctt gcc gtg gct tcc gga gct gct gcc gtg acc tat gct atc	288
Gly Gly Leu Ala Val Ala Ser Gly Ala Ala Ala Val Thr Tyr Ala Ile	
85 90 95	
gag aat atc acc cgt tcc ggt gat cat att gtg gct gcc aag acc att	336
Glu Asn Ile Thr Arg Ser Gly Asp His Ile Val Ala Ala Lys Thr Ile	
100 105 110	
tat ggg ggc aca tat aac ttg ctg gcg cat act ctg cct gct tat gga	384
Tyr Gly Gly Thr Tyr Asn Leu Leu Ala His Thr Leu Pro Ala Tyr Gly	
115 120 125	
gta acg acc act ttt gta gat ccg tcc gat ctt ttt aat ttc gaa cgg	432
Val Thr Thr Thr Phe Val Asp Pro Ser Asp Leu Phe Asn Phe Glu Arg	
130 135 140	
gcg att cgt gaa aat aca aag gcg ata ttc att gaa act ctg gga aac	480
Ala Ile Arg Glu Asn Thr Lys Ala Ile Phe Ile Glu Thr Leu Gly Asn	
145 150 155 160	
ccc aat tcc aat att atc gat atg gat gcc gta gct gcc att gcc cat	528

Pro	Asn	Ser	Asn	Ile	Ile	Asp	Met	Asp	Ala	Val	Ala	Ala	Ile	Ala	His	
				165					170					175		
aaa	tat	cgg	att	ccg	ctg	att	gtg	gat	aat	act	ttc	ggg	acg	cct	tac	576
Lys	Tyr	Arg	Ile	Pro	Leu	Ile	Val	Asp	Asn	Thr	Phe	Gly	Thr	Pro	Tyr	
			180					185				190				
ctt	atc	cgt	ccc	att	gag	cac	ggg	gca	gac	att	gtg	gta	cat	tct	gcc	624
Leu	Ile	Arg	Pro	Ile	Glu	His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Ala	
		195					200					205				
aca	aaa	ttc	att	ggc	gga	cac	ggc	agt	tcg	ttg	gga	gga	gtt	att	gtc	672
Thr	Lys	Phe	Ile	Gly	Gly	His	Gly	Ser	Ser	Leu	Gly	Gly	Val	Ile	Val	
	210					215					220					
gat	tcc	ggg	aaa	ttt	gac	tgg	gtt	gct	tcc	ggg	aaa	ttc	ccg	caa	ctg	720
Asp	Ser	Gly	Lys	Phe	Asp	Trp	Val	Ala	Ser	Gly	Lys	Phe	Pro	Gln	Leu	
225					230					235					240	
acc	gag	ccg	gat	gca	agt	tat	cat	ggg	gta	cgg	ttt	gtc	gat	gct	gcc	768
Thr	Glu	Pro	Asp	Ala	Ser	Tyr	His	Gly	Val	Arg	Phe	Val	Asp	Ala	Ala	
				245					250					255		
ggg	gct	gct	gcc	tac	att	gtc	cgt	ata	cgt	gcc	gtg	ttg	ctg	cgc	gat	816
Gly	Ala	Ala	Ala	Tyr	Ile	Val	Arg	Ile	Arg	Ala	Val	Leu	Leu	Arg	Asp	
			260					265					270			
acg	ggg	gct	gcc	atc	agc	ccg	ttc	aat	gct	ttt	atc	ttg	ctg	caa	ggg	864
Thr	Gly	Ala	Ala	Ile	Ser	Pro	Phe	Asn	Ala	Phe	Ile	Leu	Leu	Gln	Gly	
		275					280					285				
ttg	gag	act	ttg	tct	ttg	cgt	gta	gaa	cgg	cat	gtg	gcc	aat	gct	ttg	912
Leu	Glu	Thr	Leu	Ser	Leu	Arg	Val	Glu	Arg	His	Val	Ala	Asn	Ala	Leu	
	290					295					300					
aag	gtt	att	gat	ttt	ctg	gtg	aac	cat	ccg	aag	gta	gcg	gct	gtt	aat	960
Lys	Val	Ile	Asp	Phe	Leu	Val	Asn	His	Pro	Lys	Val	Ala	Ala	Val	Asn	
305					310					315					320	
cat	cca	tca	ttg	ccc	ggg	cat	ccg	gat	cat	gcc	atc	tat	caa	cgt	tat	1008
His	Pro	Ser	Leu	Pro	Gly	His	Pro	Asp	His	Ala	Ile	Tyr	Gln	Arg	Tyr	
				325					330					335		
ttt	cct	ggc	ggg	gca	ggg	tct	atc	ttc	act	ttc	gag	gta	aag	gga	gga	1056
Phe	Pro	Gly	Gly	Ala	Gly	Ser	Ile	Phe	Thr	Phe	Glu	Val	Lys	Gly	Gly	
			340					345					350			
acg	gag	gaa	gcg	cag	aag	ttt	atc	gat	agt	ctg	cag	ata	ttc	tct	ttg	1104
Thr	Glu	Glu	Ala	Gln	Lys	Phe	Ile	Asp	Ser	Leu	Gln	Ile	Phe	Ser	Leu	
		355					360					365				
ctg	gcc	aat	gtg	gcc	gat	gtg	aag	tcg	ctg	gtg	att	cat	ccg	ggc	act	1152
Leu	Ala	Asn	Val	Ala	Asp	Val	Lys	Ser	Leu	Val	Ile	His	Pro	Gly	Thr	
	370					375					380					
acc	aca	cac	tcg	cag	ttg	aat	gcg	cag	gag	ctg	gag	gaa	cag	ggg	att	1200
Thr	Thr	His	Ser	Gln	Leu	Asn	Ala	Gln	Glu	Leu	Glu	Glu	Gln	Gly	Ile	
385					390					395					400	
aaa	ccc	gga	acg	gtc	aga	ctt	tcg	ata	ggg	acg	gag	cat	att	gag	gac	1248
Lys	Pro	Gly	Thr	Val	Arg	Leu	Ser	Ile	Gly	Thr	Glu	His	Ile	Glu	Asp	
				405					410					415		
att	att	gat	gac	tta	cgt	cag	gca	tta	gag	aaa	att	taa				1287
Ile	Ile	Asp	Asp	Leu	Arg	Gln	Ala	Leu	Glu	Lys	Ile					
			420					425								

<210> 20

<211> 428

<212> PRT

<213> Bacteroides fragilis

<400> 20

Met Glu Thr Lys Lys Leu His Phe Glu Thr Leu Gln Leu His Val Gly
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Gln Glu Thr Pro Asp Pro Ala Thr Asp Ala Arg Ala Val Pro Ile Tyr
 20 25 30

Gln Thr Thr Ser Tyr Val Phe Arg Asp Ser Ala His Ala Ala Ala Arg
 35 40 45

Phe Gly Leu Gln Asp Pro Gly Asn Ile Tyr Gly Arg Leu Thr Asn Ser
 50 55 60

Thr Gln Gly Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Val
 65 70 75 80

Gly Gly Leu Ala Val Ala Ser Gly Ala Ala Ala Val Thr Tyr Ala Ile
 85 90 95

Glu Asn Ile Thr Arg Ser Gly Asp His Ile Val Ala Ala Lys Thr Ile
 100 105 110

Tyr Gly Gly Thr Tyr Asn Leu Leu Ala His Thr Leu Pro Ala Tyr Gly
 115 120 125

Val Thr Thr Thr Phe Val Asp Pro Ser Asp Leu Phe Asn Phe Glu Arg
 130 135 140

Ala Ile Arg Glu Asn Thr Lys Ala Ile Phe Ile Glu Thr Leu Gly Asn
 145 150 155 160

Pro Asn Ser Asn Ile Ile Asp Met Asp Ala Val Ala Ala Ile Ala His
 165 170 175

Lys Tyr Arg Ile Pro Leu Ile Val Asp Asn Thr Phe Gly Thr Pro Tyr
 180 185 190

Leu Ile Arg Pro Ile Glu His Gly Ala Asp Ile Val Val His Ser Ala
 195 200 205

Thr Lys Phe Ile Gly Gly His Gly Ser Ser Leu Gly Gly Val Ile Val
 210 215 220

Asp Ser Gly Lys Phe Asp Trp Val Ala Ser Gly Lys Phe Pro Gln Leu
 225 230 235 240

Thr Glu Pro Asp Ala Ser Tyr His Gly Val Arg Phe Val Asp Ala Ala
 245 250 255

Gly Ala Ala Ala Tyr Ile Val Arg Ile Arg Ala Val Leu Leu Arg Asp
 260 265 270

Thr Gly Ala Ala Ile Ser Pro Phe Asn Ala Phe Ile Leu Leu Gln Gly
 275 280 285

Leu Glu Thr Leu Ser Leu Arg Val Glu Arg His Val Ala Asn Ala Leu
 290 295 300

Lys Val Ile Asp Phe Leu Val Asn His Pro Lys Val Ala Ala Val Asn
 305 310 315 320

His Pro Ser Leu Pro Gly His Pro Asp His Ala Ile Tyr Gln Arg Tyr
 325 330 335

Phe Pro Gly Gly Ala Gly Ser Ile Phe Thr Phe Glu Val Lys Gly Gly
 340 345 350

Thr Glu Glu Ala Gln Lys Phe Ile Asp Ser Leu Gln Ile Phe Ser Leu
 355 360 365

Leu Ala Asn Val Ala Asp Val Lys Ser Leu Val Ile His Pro Gly Thr
 370 375 380

Thr Thr His Ser Gln Leu Asn Ala Gln Glu Leu Glu Glu Gln Gly Ile
 385 390 395 400

Lys Pro Gly Thr Val Arg Leu Ser Ile Gly Thr Glu His Ile Glu Asp
 405 410 415

Ile Ile Asp Asp Leu Arg Gln Ala Leu Glu Lys Ile
 420 425

<210> 21

<211> 1278

<212> DNA

<213> *Pseudomonas aeruginosa*

<220>

<221> CDS

<222> (1)..(1278)

<223>

<400> 21

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Met	Lys	Leu	Glu	Thr	Leu	Ala	Val	His	Ala	Gly	Tyr	Ser	Pro	Asp	Pro	
1				5					10					15		
acc	acc	cgc	gcg	gtg	gcg	gtg	ccg	atc	tac	cag	acc	acc	tcc	tac	gcc	96
Thr	Thr	Arg	Ala	Val	Ala	Val	Pro	Ile	Tyr	Gln	Thr	Thr	Ser	Tyr	Ala	
			20					25					30			
ttc	gac	gac	acc	cag	cat	ggc	gcc	gac	ctg	ttc	gac	ctg	aag	gta	ccg	144
Phe	Asp	Asp	Thr	Gln	His	Gly	Ala	Asp	Leu	Phe	Asp	Leu	Lys	Val	Pro	
		35					40					45				
ggc	aac	atc	tac	aca	cgg	atc	atg	aac	ccc	acc	aac	gac	gta	ctg	gaa	192
Gly	Asn	Ile	Tyr	Thr	Arg	Ile	Met	Asn	Pro	Thr	Asn	Asp	Val	Leu	Glu	
	50					55					60					
cag	cgc	gtc	gcg	gcg	ctg	gaa	ggc	ggg	gtc	ggg	gcg	ctg	gcg	gtg	gcc	240
Gln	Arg	Val	Ala	Ala	Leu	Glu	Gly	Gly	Val	Gly	Ala	Leu	Ala	Val	Ala	
65					70				75					80		
tgc	ggg	atg	gcg	gcc	atc	acc	tac	gcg	atc	cag	acc	gtc	gcc	gag	gcc	288
Ser	Gly	Met	Ala	Ala	Ile	Thr	Tyr	Ala	Ile	Gln	Thr	Val	Ala	Glu	Ala	
				85					90					95		
ggc	gac	aac	atc	gtc	tgc	gtg	gcc	aag	ctc	tac	ggc	ggc	acc	tac	aac	336
Gly	Asp	Asn	Ile	Val	Ser	Val	Ala	Lys	Leu	Tyr	Gly	Gly	Thr	Tyr	Asn	
			100					105					110			
ctg	ctg	gcc	cac	acc	ctg	cca	cgc	atc	ggc	atc	cag	gcg	cgc	ttc	gcc	384
Leu	Leu	Ala	His	Thr	Leu	Pro	Arg	Ile	Gly	Ile	Gln	Ala	Arg	Phe	Ala	
		115					120					125				
gcc	cac	gac	gac	gtc	gcc	gcc	ctg	gaa	gcg	ctg	atc	gac	gag	cgg	acc	432
Ala	His	Asp	Asp	Val	Ala	Ala	Leu	Glu	Ala	Leu	Ile	Asp	Glu	Arg	Thr	
	130					135					140					
aag	gcc	gtg	ttc	tgc	gaa	acc	atc	ggc	aac	ccg	gcg	ggc	aac	atc	atc	480
Lys	Ala	Val	Phe	Cys	Glu	Thr	Ile	Gly	Asn	Pro	Ala	Gly	Asn	Ile	Ile	
145					150					155					160	
gac	ctg	cag	gca	ctg	gcc	gac	gcc	gct	cac	cgc	cac	ggc	gtg	cca	ctg	528
Asp	Leu	Gln	Ala	Leu	Ala	Asp	Ala	Ala	His	Arg	His	Gly	Val	Pro	Leu	
				165				170						175		
atc	gtc	gac	aac	acg	gta	gcc	acc	ccg	gtg	ctc	tgc	cgg	ccg	ttc	gag	576
Ile	Val	Asp	Asn	Thr	Val	Ala	Thr	Pro	Val	Leu	Cys	Arg	Pro	Phe	Glu	
			180					185					190			
cac	ggc	gcc	gac	atc	gtc	gtg	cac	tgc	ctg	acc	aag	tac	atg	ggc	ggc	624
His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Leu	Thr	Lys	Tyr	Met	Gly	Gly	
		195					200					205				
cac	ggc	acc	agc	atc	ggc	ggg	atc	gtg	gtc	gac	tcc	ggc	aaa	ttc	gac	672
His	Gly	Thr	Ser	Ile	Gly	Gly	Ile	Val	Val	Asp	Ser	Gly	Lys	Phe	Asp	
	210					215					220					
tgg	gcg	gcg	aac	aag	tgc	cgc	ttc	ccg	ctg	ctg	aac	acg	ccc	gat	ccg	720
Trp	Ala	Ala	Asn	Lys	Ser	Arg	Phe	Pro	Leu	Leu	Asn	Thr	Pro	Asp	Pro	
225					230					235					240	

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tcc tac cac ggc gtc acc tac acc gag gcc ttc gga ccc gcc gcc ttc      768
Ser Tyr His Gly Val Thr Tyr Thr Glu Ala Phe Gly Pro Ala Ala Phe
                245                250                255

atc ggc cgc tgc cgg gtg gta ccg ctg cgc aac atg ggc gcg gcg ctc      816
Ile Gly Arg Cys Arg Val Val Pro Leu Arg Asn Met Gly Ala Ala Leu
                260                265                270

tcg ccg ttc aac gcc ttc ctc atc ctc caa ggc ctg gag acc ctg gcg      864
Ser Pro Phe Asn Ala Phe Leu Ile Leu Gln Gly Leu Glu Thr Leu Ala
                275                280                285

ctg cgc atg gag cgc cac tgc gac aac gcc ctc gcc gtg gcc cgc tac      912
Leu Arg Met Glu Arg His Cys Asp Asn Ala Leu Ala Val Ala Arg Tyr
                290                295                300

ctg cag cag cat ccg cag gtg gcc tgg gtg aaa tac gcc ggc ctc gcc      960
Leu Gln Gln His Pro Gln Val Ala Trp Val Lys Tyr Ala Gly Leu Ala
                305                310                315                320

gac aac ccc gag cac gcc ctg gcc cgg cgc tac ctg ggg ggc cgc ccg      1008
Asp Asn Pro Glu His Ala Leu Ala Arg Arg Tyr Leu Gly Gly Arg Pro
                325                330                335

gcg gcg atc ctg tct ttc ggc atc cag ggc ggc agc gcc gcc ggc gcg      1056
Ala Ala Ile Leu Ser Phe Gly Ile Gln Gly Gly Ser Ala Ala Gly Ala
                340                345                350

cgc ttc atc gac gcc ttg aag ctg gtg gtg cgg ctg gtc aac atc ggc      1104
Arg Phe Ile Asp Ala Leu Lys Leu Val Val Arg Leu Val Asn Ile Gly
                355                360                365

gac gcc aag tcc ctg gcc tgc cac ccg gcg agc acc acc cac cgc cag      1152
Asp Ala Lys Ser Leu Ala Cys His Pro Ala Ser Thr Thr His Arg Gln
                370                375                380

ttg aac gcg gag gaa ctg gcc cgc gcc gga gtc tcc gac gac atg gtg      1200
Leu Asn Ala Glu Glu Leu Ala Arg Ala Gly Val Ser Asp Asp Met Val
                385                390                395                400

cgg ctg tcg atc ggc atc gag cac atc gac gac atc ctc gcc gac ctc      1248
Arg Leu Ser Ile Gly Ile Glu His Ile Asp Asp Ile Leu Ala Asp Leu
                405                410                415

gac cag gcc ctg gcc gcc gcc gca cgc tga      1278
Asp Gln Ala Leu Ala Ala Ala Ala Arg
                420                425

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<210> 22

<211> 425

<212> PRT

<213> Pseudomonas aeruginosa

<400> 22

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Met Lys Leu Glu Thr Leu Ala Val His Ala Gly Tyr Ser Pro Asp Pro
1          5          10          15

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Thr Thr Arg Ala Val Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Ala

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Gly	Asn	Ile	Tyr	Thr	Arg	Ile	Met	Asn	Pro	Thr	Asn	Asp	Val	Leu	Glu
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Gln	Arg	Val	Ala	Ala	Leu	Glu	Gly	Gly	Val	Gly	Ala	Leu	Ala	Val	Ala
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Ser	Gly	Met	Ala	Ala	Ile	Thr	Tyr	Ala	Ile	Gln	Thr	Val	Ala	Glu	Ala
			85						90					95	
Gly	Asp	Asn	Ile	Val	Ser	Val	Ala	Lys	Leu	Tyr	Gly	Gly	Thr	Tyr	Asn
			100					105					110		
Leu	Leu	Ala	His	Thr	Leu	Pro	Arg	Ile	Gly	Ile	Gln	Ala	Arg	Phe	Ala
		115					120					125			
Ala	His	Asp	Asp	Val	Ala	Ala	Leu	Glu	Ala	Leu	Ile	Asp	Glu	Arg	Thr
	130					135					140				
Lys	Ala	Val	Phe	Cys	Glu	Thr	Ile	Gly	Asn	Pro	Ala	Gly	Asn	Ile	Ile
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Asp	Leu	Gln	Ala	Leu	Ala	Asp	Ala	Ala	His	Arg	His	Gly	Val	Pro	Leu
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Ile	Val	Asp	Asn	Thr	Val	Ala	Thr	Pro	Val	Leu	Cys	Arg	Pro	Phe	Glu
			180					185					190		
His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Leu	Thr	Lys	Tyr	Met	Gly	Gly
		195					200					205			
His	Gly	Thr	Ser	Ile	Gly	Gly	Ile	Val	Val	Asp	Ser	Gly	Lys	Phe	Asp
	210					215					220				
Trp	Ala	Ala	Asn	Lys	Ser	Arg	Phe	Pro	Leu	Leu	Asn	Thr	Pro	Asp	Pro
225					230					235					240
Ser	Tyr	His	Gly	Val	Thr	Tyr	Thr	Glu	Ala	Phe	Gly	Pro	Ala	Ala	Phe
				245					250					255	
Ile	Gly	Arg	Cys	Arg	Val	Val	Pro	Leu	Arg	Asn	Met	Gly	Ala	Ala	Leu
			260					265					270		
Ser	Pro	Phe	Asn	Ala	Phe	Leu	Ile	Leu	Gln	Gly	Leu	Glu	Thr	Leu	Ala
		275					280					285			

Leu Arg Met Glu Arg His Cys Asp Asn Ala Leu Ala Val Ala Arg Tyr
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Leu Gln Gln His Pro Gln Val Ala Trp Val Lys Tyr Ala Gly Leu Ala
 305 310 315 320

Asp Asn Pro Glu His Ala Leu Ala Arg Arg Tyr Leu Gly Gly Arg Pro
 325 330 335

Ala Ala Ile Leu Ser Phe Gly Ile Gln Gly Gly Ser Ala Ala Gly Ala
 340 345 350

Arg Phe Ile Asp Ala Leu Lys Leu Val Val Arg Leu Val Asn Ile Gly
 355 360 365

Asp Ala Lys Ser Leu Ala Cys His Pro Ala Ser Thr Thr His Arg Gln
 370 375 380

Leu Asn Ala Glu Glu Leu Ala Arg Ala Gly Val Ser Asp Asp Met Val
 385 390 395 400

Arg Leu Ser Ile Gly Ile Glu His Ile Asp Asp Ile Leu Ala Asp Leu
 405 410 415

Asp Gln Ala Leu Ala Ala Ala Ala Arg
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<210> 23

<211> 1296

<212> DNA

<213> Bordetella bronchiseptica

<220>

<221> CDS

<222> (1)..(1296)

<223>

<400> 23

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cat ggg ggc tac cgg ccc gac ccg acc acg cgc gcg gtg gcg gtg ccg 96
 His Gly Gly Tyr Arg Pro Asp Pro Thr Thr Arg Ala Val Ala Val Pro
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atc tac cag acc gtg gcc tat gcg ttc gac gac acc cag cat ggc gcg 144
 Ile Tyr Gln Thr Val Ala Tyr Ala Phe Asp Asp Thr Gln His Gly Ala

35	40	45	
gac ctg ttc gac ctg aag gtg ccg ggc aat atc tac acc cgc atc atg Asp Leu Phe Asp Leu Lys Val Pro Gly Asn Ile Tyr Thr Arg Ile Met 50 55 60			192
aac ccc acc acc gac gtg ctg gag cag cgc gtg gcg gcg ctg gaa tgc Asn Pro Thr Thr Asp Val Leu Glu Gln Arg Val Ala Ala Leu Glu Cys 65 70 75 80			240
ggc gtg gcc gcg ctg gcg ctg gcc tcc ggc cag gcg gcg gtg acc tat Gly Val Ala Ala Leu Ala Leu Ala Ser Gly Gln Ala Ala Val Thr Tyr 85 90 95			288
gcg atc ctg acc atc gcc gag gcg ggc gac aac atc gtg tcg tcc agc Ala Ile Leu Thr Ile Ala Glu Ala Gly Asp Asn Ile Val Ser Ser Ser 100 105 110			336
acg ctg tat ggc ggc acg tac aac ctg ttc gcc cac acg ctg ccg cag Thr Leu Tyr Gly Gly Thr Tyr Asn Leu Phe Ala His Thr Leu Pro Gln 115 120 125			384
tac ggc atc acg acc cgc ttc gcc gat ccg cgc aac ctg gct tcg ttc Tyr Gly Ile Thr Thr Arg Phe Ala Asp Pro Arg Asn Leu Ala Ser Phe 130 135 140			432
gag gcg ctg atc gac gag cgc acc aag gcc att ttc gcc gag tcg gtg Glu Ala Leu Ile Asp Glu Arg Thr Lys Ala Ile Phe Ala Glu Ser Val 145 150 155 160			480
ggc aat ccg ctg ggc aac gtc acc gac atc gcc gcg ctg gcc gag atc Gly Asn Pro Leu Gly Asn Val Thr Asp Ile Ala Ala Leu Ala Glu Ile 165 170 175			528
gcg cac cgc cat ggc gtg ccg ctg atc gtc gac aac acg gtg ccg tcg Ala His Arg His Gly Val Pro Leu Ile Val Asp Asn Thr Val Pro Ser 180 185 190			576
ccc tac ctg ctg cgc ccc atc gag cac ggc gcc gac atc gtg gtg cag Pro Tyr Leu Leu Arg Pro Ile Glu His Gly Ala Asp Ile Val Val Gln 195 200 205			624
tcg ctc acc aag tac ctg ggc ggg cac ggc acc agc ctg ggc ggg gcc Ser Leu Thr Lys Tyr Leu Gly Gly His Gly Thr Ser Leu Gly Gly Ala 210 215 220			672
atc atc gat tcg ggc aag ttt ccc tgg gcc gag cac aag gcg cgc ttc Ile Ile Asp Ser Gly Lys Phe Pro Trp Ala Glu His Lys Ala Arg Phe 225 230 235 240			720
aag cgc ctg aac gag ccc gac gtg agc tac cac ggc gtg gtc tac acc Lys Arg Leu Asn Glu Pro Asp Val Ser Tyr His Gly Val Val Tyr Thr 245 250 255			768
gag gcg ttc ggc gcg gcg gcc tat atc ggc cgc gcc cgc gtg gtg ccg Glu Ala Phe Gly Ala Ala Ala Tyr Ile Gly Arg Ala Arg Val Val Pro 260 265 270			816
ctg cgc aat acc ggc gcg gcc att tcg ccg ttc aac gcc ttc cag atc Leu Arg Asn Thr Gly Ala Ala Ile Ser Pro Phe Asn Ala Phe Gln Ile 275 280 285			864
ctg cag ggc atc gag acg ctg gcg ctg cgc gtg gac cgc atc gtc gag Leu Gln Gly Ile Glu Thr Leu Ala Leu Arg Val Asp Arg Ile Val Glu 290 295 300			912
aac tcg gtc aag gtg gcc ggg ttc ctg cgc gac cat ccc aag gtc gaa			960

Asn 305	Ser	Val	Lys	Val	Ala 310	Gly	Phe	Leu	Arg	Asp 315	His	Pro	Lys	Val	Glu 320	
tgg	gtc	aac	tat	gcc	ggc	ctg	ccc	gac	cat	gcc	gac	cat	gcg	ctg	gtg	1008
Trp	Val	Asn	Tyr	Ala 325	Gly	Leu	Pro	Asp	His 330	Ala	Asp	His	Ala	Leu	Val 335	
cgc	aag	tac	atg	ggc	ggc	aag	gcc	ccc	ggc	ctg	ttc	act	ttc	ggc	gtg	1056
Arg	Lys	Tyr	Met 340	Gly	Gly	Lys	Ala	Pro 345	Gly	Leu	Phe	Thr	Phe	Gly	Val 350	
aag	ggc	ggc	cgc	gag	gcc	ggc	gcg	cgc	ttc	cag	gac	gcc	ttg	cag	ctg	1104
Lys	Gly	Gly	Arg 355	Glu	Ala	Gly	Ala	Arg 360	Phe	Gln	Asp	Ala	Leu	Gln	Leu 365	
ttc	acc	cgc	ctg	gtg	aac	atc	ggc	gac	gcc	aag	tcg	ctg	gcc	acg	cac	1152
Phe	Thr	Arg	Leu 370	Val	Asn 375	Ile	Gly	Asp	Ala	Lys	Ser 380	Leu	Ala	Thr	His	
ccg	gct	tcc	acc	acg	cac	cgc	cag	ctc	aac	ccc	gaa	gag	ctc	gaa	aag	1200
Pro	Ala	Ser	Thr	Thr	His 390	Arg	Gln	Leu	Asn 395	Pro	Glu	Glu	Leu	Glu	Lys 400	
gcc	ggc	gtg	cgc	gag	gaa	acg	gtg	cgc	ctg	tcg	atc	ggg	atc	gag	cat	1248
Ala	Gly	Val	Arg 405	Glu	Glu	Thr	Val	Arg 410	Leu	Ser	Ile	Gly	Ile	Glu	His 415	
atc	gac	gac	ctg	atc	gcc	gac	ctg	gaa	cag	gcg	ctg	gcg	caa	gtc	tga	1296
Ile	Asp	Asp	Leu 420	Ile	Ala	Asp	Leu 425	Glu	Gln	Ala	Leu	Ala	Gln	Val 430		

<210> 24

<211> 431

<212> PRT

<213> Bordetella bronchiseptica

<400> 24

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His	Gly	Gly	Tyr 20	Arg	Pro	Asp	Pro	Thr 25	Thr	Arg	Ala	Val	Ala 30	Val	Pro
Ile	Tyr	Gln	Thr 35	Val	Ala	Tyr	Ala 40	Phe	Asp	Asp	Thr	Gln 45	His	Gly	Ala
Asp	Leu	Phe	Asp 50	Leu	Lys	Val 55	Pro	Gly	Asn	Ile	Tyr 60	Thr	Arg	Ile	Met
Asn 65	Pro	Thr	Thr	Asp	Val 70	Leu	Glu	Gln	Arg 75	Val	Ala	Ala	Leu	Glu	Cys 80
Gly	Val	Ala	Ala	Leu 85	Ala	Leu	Ala	Ser	Gly 90	Gln	Ala	Ala	Val	Thr	Tyr 95

Ala Ile Leu Thr Ile Ala Glu Ala Gly Asp Asn Ile Val Ser Ser Ser
 100 105 110
 Thr Leu Tyr Gly Gly Thr Tyr Asn Leu Phe Ala His Thr Leu Pro Gln
 115 120 125
 Tyr Gly Ile Thr Thr Arg Phe Ala Asp Pro Arg Asn Leu Ala Ser Phe
 130 135 140
 Glu Ala Leu Ile Asp Glu Arg Thr Lys Ala Ile Phe Ala Glu Ser Val
 145 150 155 160
 Gly Asn Pro Leu Gly Asn Val Thr Asp Ile Ala Ala Leu Ala Glu Ile
 165 170 175
 Ala His Arg His Gly Val Pro Leu Ile Val Asp Asn Thr Val Pro Ser
 180 185 190
 Pro Tyr Leu Leu Arg Pro Ile Glu His Gly Ala Asp Ile Val Val Gln
 195 200 205
 Ser Leu Thr Lys Tyr Leu Gly Gly His Gly Thr Ser Leu Gly Gly Ala
 210 215 220
 Ile Ile Asp Ser Gly Lys Phe Pro Trp Ala Glu His Lys Ala Arg Phe
 225 230 235 240
 Lys Arg Leu Asn Glu Pro Asp Val Ser Tyr His Gly Val Val Tyr Thr
 245 250 255
 Glu Ala Phe Gly Ala Ala Ala Tyr Ile Gly Arg Ala Arg Val Val Pro
 260 265 270
 Leu Arg Asn Thr Gly Ala Ala Ile Ser Pro Phe Asn Ala Phe Gln Ile
 275 280 285
 Leu Gln Gly Ile Glu Thr Leu Ala Leu Arg Val Asp Arg Ile Val Glu
 290 295 300
 Asn Ser Val Lys Val Ala Gly Phe Leu Arg Asp His Pro Lys Val Glu
 305 310 315 320
 Trp Val Asn Tyr Ala Gly Leu Pro Asp His Ala Asp His Ala Leu Val
 325 330 335
 Arg Lys Tyr Met Gly Gly Lys Ala Pro Gly Leu Phe Thr Phe Gly Val
 340 345 350
 Lys Gly Gly Arg Glu Ala Gly Ala Arg Phe Gln Asp Ala Leu Gln Leu
 355 360 365

Phe Thr Arg Leu Val Asn Ile Gly Asp Ala Lys Ser Leu Ala Thr His
 370 375 380

Pro Ala Ser Thr Thr His Arg Gln Leu Asn Pro Glu Glu Leu Glu Lys
 385 390 395 400

Ala Gly Val Arg Glu Glu Thr Val Arg Leu Ser Ile Gly Ile Glu His
 405 410 415

Ile Asp Asp Leu Ile Ala Asp Leu Glu Gln Ala Leu Ala Gln Val
 420 425 430

<210> 25

<211> 1269

<212> DNA

<213> Nitrosomonas europaea

<220>

<221> CDS

<222> (1)..(1269)

<223>

<400> 25

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cag	act	cat	gca	gtc	gcg	gtc	ccc	att	tac	cag	acc	acc	agc	tac	tat	96
Gln	Thr	His	Ala	Val	Ala	Val	Pro	Ile	Tyr	Gln	Thr	Thr	Ser	Tyr	Tyr	
			20					25					30			
ttt	gat	gat	act	cag	cac	ggg	gct	gat	ttg	ttt	gat	ctg	aag	gtg	cag	144
Phe	Asp	Asp	Thr	Gln	His	Gly	Ala	Asp	Leu	Phe	Asp	Leu	Lys	Val	Gln	
		35					40					45				
ggt	aac	atc	tac	aca	cgc	atc	atg	aac	ccg	act	act	gct	gtc	ctg	gaa	192
Gly	Asn	Ile	Tyr	Thr	Arg	Ile	Met	Asn	Pro	Thr	Thr	Ala	Val	Leu	Glu	
	50					55					60					
gaa	aga	gtg	gcg	tta	ctg	gaa	gga	gga	gtg	gga	gcg	ctg	gcc	atg	gct	240
Glu	Arg	Val	Ala	Leu	Leu	Glu	Gly	Gly	Val	Gly	Ala	Leu	Ala	Met	Ala	
65					70				75					80		
tcc	ggc	atg	gcc	gcc	att	aca	gcc	tgt	gtg	cag	act	ctg	gcc	agg	gcg	288
Ser	Gly	Met	Ala	Ala	Ile	Thr	Ala	Cys	Val	Gln	Thr	Leu	Ala	Arg	Ala	
				85				90						95		
ggc	gac	aac	att	atc	tcc	acc	agc	cag	gtt	tac	ggt	ggc	acc	tat	aat	336
Gly	Asp	Asn	Ile	Ile	Ser	Thr	Ser	Gln	Val	Tyr	Gly	Gly	Thr	Tyr	Asn	
			100					105						110		

ttc ttt tgc cat acg ttg ccc aat ctg ggt att gaa gtt cgc atg gtg Phe Phe Cys His Thr Leu Pro Asn Leu Gly Ile Glu Val Arg Met Val 115 120 125	384
gat ggt cgt aat ccg gcc gct ttt gcc gat gcc atc gat gac aat acc Asp Gly Arg Asn Pro Ala Ala Phe Ala Asp Ala Ile Asp Asp Asn Thr 130 135 140	432
aga atg att tat tgc gag tcg atc gga aat ccg gcc ggt aat gtg gtg Arg Met Ile Tyr Cys Glu Ser Ile Gly Asn Pro Ala Gly Asn Val Val 145 150 155 160	480
gat atc gcc gca ctg gct gaa gtg gcg cat gca gcg ggc gtg ccg ctg Asp Ile Ala Ala Leu Ala Glu Val Ala His Ala Ala Gly Val Pro Leu 165 170 175	528
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cat ggt gcc gat atc gtc gtc cat gcg ctg acc aaa tac atg ggt ggt His Gly Ala Asp Ile Val Val His Ala Leu Thr Lys Tyr Met Gly Gly 195 200 205	624
cac ggc acc agc atc ggc gga atc atc gtg gat tcc ggc aag ttc ccc His Gly Thr Ser Ile Gly Gly Ile Ile Val Asp Ser Gly Lys Phe Pro 210 215 220	672
tgg gaa ggc aac tcg cgt ttt cca caa ttc aac caa cct gat ccc agc Trp Glu Gly Asn Ser Arg Phe Pro Gln Phe Asn Gln Pro Asp Pro Ser 225 230 235 240	720
tat cac ggt gtg gtt tat gtg gat gca ttt ggt ccg gct gcg ttt atc Tyr His Gly Val Tyr Val Asp Ala Phe Gly Pro Ala Ala Phe Ile 245 250 255	768
ggc cgt gcg cgt gtg gta ccg ttg cgc aac atg gga gcg gca att tca Gly Arg Ala Arg Val Val Pro Leu Arg Asn Met Gly Ala Ala Ile Ser 260 265 270	816
cct ttc aat tct ttt ctg att ctg caa ggt atc gaa acc ctg ccg ttg Pro Phe Asn Ser Phe Leu Ile Leu Gln Gly Ile Glu Thr Leu Pro Leu 275 280 285	864
agg atg gaa cgg cat tgc acc aat gcg ctg gcg att gca cgt tat ctg Arg Met Glu Arg His Cys Thr Asn Ala Leu Ala Ile Ala Arg Tyr Leu 290 295 300	912
caa agg cat ccc aaa gtc agc tgg gtc aat ttt gcc ggc ctt gaa gat Gln Arg His Pro Lys Val Ser Trp Val Asn Phe Ala Gly Leu Glu Asp 305 310 315 320	960
aac cgt gat tac gca ctg gtg cag aaa tac atg gat ggc ggt att ccc Asn Arg Asp Tyr Ala Leu Val Gln Lys Tyr Met Asp Gly Gly Ile Pro 325 330 335	1008
tca tcg att ctg agt ttt ggc atc aag ggc ggg cgc gag gct tgt gct Ser Ser Ile Leu Ser Phe Gly Ile Lys Gly Gly Arg Glu Ala Cys Ala 340 345 350	1056
cgc ttt atg gac aga ctg atg ctg atc aaa ccg ctg gtc aac atc ggg Arg Phe Met Asp Arg Leu Met Leu Ile Lys Arg Leu Val Asn Ile Gly 355 360 365	1104
gat gcc aaa acg ctg gcc tgc cac ccg gcg acg acc acc cac cgt cag Asp Ala Lys Thr Leu Ala Cys His Pro Ala Thr Thr Thr His Arg Gln 370 375 380	1152

ctc aat gat gaa gaa ctg gca aaa gcc ggt gtc agt gct gat ctg gtg 1200
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 385 390 395 400

cgt tta tgt gtc ggc atc gag cat att gac gat ctg att gcc gat gta 1248
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 405 410 415

gag cag gct ttc cag gat tag 1269
 Glu Gln Ala Phe Gln Asp
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<210> 26

<211> 422

<212> PRT

<213> Nitrosomonas europaea

<400> 26

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Phe Asp Asp Thr Gln His Gly Ala Asp Leu Phe Asp Leu Lys Val Gln
 35 40 45

Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Thr Ala Val Leu Glu
 50 55 60

Glu Arg Val Ala Leu Leu Glu Gly Gly Val Gly Ala Leu Ala Met Ala
 65 70 75 80

Ser Gly Met Ala Ala Ile Thr Ala Cys Val Gln Thr Leu Ala Arg Ala
 85 90 95

Gly Asp Asn Ile Ile Ser Thr Ser Gln Val Tyr Gly Gly Thr Tyr Asn
 100 105 110

Phe Phe Cys His Thr Leu Pro Asn Leu Gly Ile Glu Val Arg Met Val
 115 120 125

Asp Gly Arg Asn Pro Ala Ala Phe Ala Asp Ala Ile Asp Asp Asn Thr
 130 135 140

Arg Met Ile Tyr Cys Glu Ser Ile Gly Asn Pro Ala Gly Asn Val Val
 145 150 155 160

Asp Ile Ala Ala Leu Ala Glu Val Ala His Ala Ala Gly Val Pro Leu

165					170					175					
Val	Val	Asp	Asn	Thr	Val	Pro	Thr	Pro	Val	Leu	Cys	Arg	Pro	Phe	Glu
			180					185					190		
His	Gly	Ala	Asp	Ile	Val	Val	His	Ala	Leu	Thr	Lys	Tyr	Met	Gly	Gly
		195					200					205			
His	Gly	Thr	Ser	Ile	Gly	Gly	Ile	Ile	Val	Asp	Ser	Gly	Lys	Phe	Pro
	210					215					220				
Trp	Glu	Gly	Asn	Ser	Arg	Phe	Pro	Gln	Phe	Asn	Gln	Pro	Asp	Pro	Ser
225						230					235				240
Tyr	His	Gly	Val	Val	Tyr	Val	Asp	Ala	Phe	Gly	Pro	Ala	Ala	Phe	Ile
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Gly	Arg	Ala	Arg	Val	Val	Pro	Leu	Arg	Asn	Met	Gly	Ala	Ala	Ile	Ser
			260					265						270	
Pro	Phe	Asn	Ser	Phe	Leu	Ile	Leu	Gln	Gly	Ile	Glu	Thr	Leu	Pro	Leu
		275					280					285			
Arg	Met	Glu	Arg	His	Cys	Thr	Asn	Ala	Leu	Ala	Ile	Ala	Arg	Tyr	Leu
	290					295					300				
Gln	Arg	His	Pro	Lys	Val	Ser	Trp	Val	Asn	Phe	Ala	Gly	Leu	Glu	Asp
305						310					315				320
Asn	Arg	Asp	Tyr	Ala	Leu	Val	Gln	Lys	Tyr	Met	Asp	Gly	Gly	Ile	Pro
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Ser	Ser	Ile	Leu	Ser	Phe	Gly	Ile	Lys	Gly	Gly	Arg	Glu	Ala	Cys	Ala
			340					345					350		
Arg	Phe	Met	Asp	Arg	Leu	Met	Leu	Ile	Lys	Arg	Leu	Val	Asn	Ile	Gly
		355					360					365			
Asp	Ala	Lys	Thr	Leu	Ala	Cys	His	Pro	Ala	Thr	Thr	Thr	His	Arg	Gln
	370					375					380				
Leu	Asn	Asp	Glu	Glu	Leu	Ala	Lys	Ala	Gly	Val	Ser	Ala	Asp	Leu	Val
385						390					395				400
Arg	Leu	Cys	Val	Gly	Ile	Glu	His	Ile	Asp	Asp	Leu	Ile	Ala	Asp	Val
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<210> 27

<211> 1281

<212> DNA

<213> Sinorhizobium meliloti

<220>

<221> CDS

<222> (1)..(1281)

<223>

<400> 27

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cag ccc gat ccg acg acc ggt gcg cgg gcg acg ccg atc tat cag acg	96
Gln Pro Asp Pro Thr Thr Gly Ala Arg Ala Thr Pro Ile Tyr Gln Thr	
20 25 30	
acc agc ttc gtc ttc aac gac acg gat cat gcg gcc gca ctc ttc ggc	144
Thr Ser Phe Val Phe Asn Asp Thr Asp His Ala Ala Ala Leu Phe Gly	
35 40 45	
ctc cag caa ttc ggc aat atc tat acc cgc atc atg aat ccg acg cag	192
Leu Gln Gln Phe Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Gln	
50 55 60	
gcg gtg ctg gag gag cgg atc gcg gcg ctc gaa ggc ggg acc gcc ggg	240
Ala Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Thr Ala Gly	
65 70 75 80	
ctg gcc gtt tcc tcg ggg cat gcg gcc cag ctg ctg gtt ttc cat acg	288
Leu Ala Val Ser Ser Gly His Ala Ala Gln Leu Leu Val Phe His Thr	
85 90 95	
atc atg agg ccg ggt gac aat ttc gtt tcc gcc aga cag ctt tac ggc	336
Ile Met Arg Pro Gly Asp Asn Phe Val Ser Ala Arg Gln Leu Tyr Gly	
100 105 110	
ggg tcg gcc aat cag ttc ggc cat gcc ttc aag gcc ttc gac tgg cag	384
Gly Ser Ala Asn Gln Phe Gly His Ala Phe Lys Ala Phe Asp Trp Gln	
115 120 125	
gtc cgc tgg gcc gat tcg gcg gag ccc gaa agc ttc gat gcg cag atc	432
Val Arg Trp Ala Asp Ser Ala Glu Pro Glu Ser Phe Asp Ala Gln Ile	
130 135 140	
gac gaa cgc acc aag gcg atc ttc atc gaa agc ctc gcc aat ccg ggc	480
Asp Glu Arg Thr Lys Ala Ile Phe Ile Glu Ser Leu Ala Asn Pro Gly	
145 150 155 160	
ggc acc ttc gtc gac ata gcc gca atc gct gac gtt gcg cgg cga cac	528
Gly Thr Phe Val Asp Ile Ala Ala Ile Ala Asp Val Ala Arg Arg His	
165 170 175	
gga ctg ccg ctc atc gtc gac aat acg atg gcg acg ccc tat ctg atg	576

Gly	Leu	Pro	Leu	Ile	Val	Asp	Asn	Thr	Met	Ala	Thr	Pro	Tyr	Leu	Met	
			180					185					190			
cgg	ccg	ctc	gaa	cac	ggc	gcc	gat	atc	gtc	gtc	cat	tcg	ctc	acc	aag	624
Arg	Pro	Leu	Glu	His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Leu	Thr	Lys	
		195					200					205				
ttc	atc	ggc	ggt	cac	ggc	aat	tcg	atg	ggc	ggc	atc	atc	gtc	gac	ggc	672
Phe	Ile	Gly	Gly	His	Gly	Asn	Ser	Met	Gly	Gly	Ile	Ile	Val	Asp	Gly	
	210					215					220					
ggt	acg	ttc	gac	tgg	tcg	aaa	tcc	ggc	aag	tat	ccg	ctg	ctg	tcg	gag	720
Gly	Thr	Phe	Asp	Trp	Ser	Lys	Ser	Gly	Lys	Tyr	Pro	Leu	Leu	Ser	Glu	
225				230						235					240	
ccg	agg	ccc	gaa	tat	ggc	ggc	gtc	gtc	ctg	cac	cag	gcc	ttc	ggc	aac	768
Pro	Arg	Pro	Glu	Tyr	Gly	Gly	Val	Val	Leu	His	Gln	Ala	Phe	Gly	Asn	
				245					250					255		
ttc	gcc	ttc	gcc	atc	gcc	gca	cgg	gta	ttg	ggt	ctg	agg	gac	ttc	ggt	816
Phe	Ala	Phe	Ala	Ile	Ala	Ala	Arg	Val	Leu	Gly	Leu	Arg	Asp	Phe	Gly	
			260					265					270			
ccg	gcc	att	tcg	ccc	ttc	aac	gcc	ttc	ctg	atc	cag	acc	ggc	gtc	gag	864
Pro	Ala	Ile	Ser	Pro	Phe	Asn	Ala	Phe	Leu	Ile	Gln	Thr	Gly	Val	Glu	
		275					280					285				
acg	ctg	ccg	ctg	agg	atg	cag	cgc	cat	tgc	gac	aac	gcg	ctg	gag	gtc	912
Thr	Leu	Pro	Leu	Arg	Met	Gln	Arg	His	Cys	Asp	Asn	Ala	Leu	Glu	Val	
	290					295					300					
gcc	aaa	tgg	ctg	aag	gga	cat	gaa	aag	gtc	tcc	tgg	gtc	cgc	tat	tcc	960
Ala	Lys	Trp	Leu	Lys	Gly	His	Glu	Lys	Val	Ser	Trp	Val	Arg	Tyr	Ser	
305					310				315						320	
ggg	ctc	gaa	gac	gat	ccg	aac	cac	gca	ctg	cag	aaa	cgc	tac	tcg	ccg	1008
Gly	Leu	Glu	Asp	Asp	Pro	Asn	His	Ala	Leu	Gln	Lys	Arg	Tyr	Ser	Pro	
				325					330					335		
aag	ggg	gcg	gga	gcc	gtt	ttc	acc	ttc	ggg	ctc	gcg	ggc	gga	tac	gag	1056
Lys	Gly	Ala	Gly	Ala	Val	Phe	Thr	Phe	Gly	Leu	Ala	Gly	Gly	Tyr	Glu	
			340					345					350			
gcg	gga	aag	cgc	ttt	gtc	gag	gca	ctg	gaa	atg	ttc	tcc	cat	ctt	gcc	1104
Ala	Gly	Lys	Arg	Phe	Val	Glu	Ala	Leu	Glu	Met	Phe	Ser	His	Leu	Ala	
		355					360					365				
aat	atc	ggc	gac	acg	cgt	tcg	ctc	gtc	atc	cac	ccc	gca	tcg	acc	acg	1152
Asn	Ile	Gly	Asp	Thr	Arg	Ser	Leu	Val	Ile	His	Pro	Ala	Ser	Thr	Thr	
	370					375					380					
cac	ccg	cag	ctc	acg	ccg	gag	cag	cag	gtc	gcc	gca	ggc	gcc	gga	ccc	1200
His	Arg	Gln	Leu	Thr	Pro	Glu	Gln	Gln	Val	Ala	Ala	Gly	Ala	Gly	Pro	
					390					395					400	
gac	gtc	atc	cgg	ttg	tcg	gtc	ggc	atc	gag	gat	gtg	gcc	gac	atc	att	1248
Asp	Val	Ile	Arg	Leu	Ser	Val	Gly	Ile	Glu	Asp	Val	Ala	Asp	Ile	Ile	
				405					410					415		
gcc	gat	ctc	gaa	cag	gcg	ctg	ggc	aag	gcc	tga						1281
Ala	Asp	Leu	Glu	Gln	Ala	Leu	Gly	Lys	Ala							
			420					425								

<210> 28

<211> 426

<212> PRT

<213> Sinorhizobium meliloti

<400> 28

Met Lys Ala Gly Pro Gly Phe Ser Thr Leu Ala Ile His Ala Gly Ala
 1 5 10 15

Gln Pro Asp Pro Thr Thr Gly Ala Arg Ala Thr Pro Ile Tyr Gln Thr
 20 25 30

Thr Ser Phe Val Phe Asn Asp Thr Asp His Ala Ala Ala Leu Phe Gly
 35 40 45

Leu Gln Gln Phe Gly Asn Ile Tyr Thr Arg Ile Met Asn Pro Thr Gln
 50 55 60

Ala Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Thr Ala Gly
 65 70 75 80

Leu Ala Val Ser Ser Gly His Ala Ala Gln Leu Leu Val Phe His Thr
 85 90 95

Ile Met Arg Pro Gly Asp Asn Phe Val Ser Ala Arg Gln Leu Tyr Gly
 100 105 110

Gly Ser Ala Asn Gln Phe Gly His Ala Phe Lys Ala Phe Asp Trp Gln
 115 120 125

Val Arg Trp Ala Asp Ser Ala Glu Pro Glu Ser Phe Asp Ala Gln Ile
 130 135 140

Asp Glu Arg Thr Lys Ala Ile Phe Ile Glu Ser Leu Ala Asn Pro Gly
 145 150 155 160

Gly Thr Phe Val Asp Ile Ala Ala Ile Ala Asp Val Ala Arg Arg His
 165 170 175

Gly Leu Pro Leu Ile Val Asp Asn Thr Met Ala Thr Pro Tyr Leu Met
 180 185 190

Arg Pro Leu Glu His Gly Ala Asp Ile Val Val His Ser Leu Thr Lys
 195 200 205

Phe Ile Gly Gly His Gly Asn Ser Met Gly Gly Ile Ile Val Asp Gly
 210 215 220

Gly Thr Phe Asp Trp Ser Lys Ser Gly Lys Tyr Pro Leu Leu Ser Glu
 225 230 235 240

Pro Arg Pro Glu Tyr Gly Gly Val Val Leu His Gln Ala Phe Gly Asn
 245 250 255

 Phe Ala Phe Ala Ile Ala Ala Arg Val Leu Gly Leu Arg Asp Phe Gly
 260 265 270

 Pro Ala Ile Ser Pro Phe Asn Ala Phe Leu Ile Gln Thr Gly Val Glu
 275 280 285

 Thr Leu Pro Leu Arg Met Gln Arg His Cys Asp Asn Ala Leu Glu Val
 290 295 300

 Ala Lys Trp Leu Lys Gly His Glu Lys Val Ser Trp Val Arg Tyr Ser
 305 310 315 320

 Gly Leu Glu Asp Asp Pro Asn His Ala Leu Gln Lys Arg Tyr Ser Pro
 325 330 335

 Lys Gly Ala Gly Ala Val Phe Thr Phe Gly Leu Ala Gly Gly Tyr Glu
 340 345 350

 Ala Gly Lys Arg Phe Val Glu Ala Leu Glu Met Phe Ser His Leu Ala
 355 360 365

 Asn Ile Gly Asp Thr Arg Ser Leu Val Ile His Pro Ala Ser Thr Thr
 370 375 380

 His Arg Gln Leu Thr Pro Glu Gln Gln Val Ala Ala Gly Ala Gly Pro
 385 390 395 400

 Asp Val Ile Arg Leu Ser Val Gly Ile Glu Asp Val Ala Asp Ile Ile
 405 410 415

 Ala Asp Leu Glu Gln Ala Leu Gly Lys Ala
 420 425

<210> 29

<211> 1293

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)..(1293)

<223>

<400>	29															
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Met	Asp	Trp	Lys	Lys	Tyr	Gly	Tyr	Asn	Thr	Arg	Ala	Leu	His	Ala	Gly	
1			5						10					15		
tat	gaa	cca	ccc	gag	cag	gcc	aca	gga	tcg	aga	gcg	gtc	cct	ata	tat	96
Tyr	Glu	Pro	Pro	Glu	Gln	Ala	Thr	Gly	Ser	Arg	Ala	Val	Pro	Ile	Tyr	
			20					25					30			
caa	acg	act	tct	tac	gtt	ttc	aga	gac	tct	gat	cac	gcg	gcg	aga	ctc	144
Gln	Thr	Thr	Ser	Tyr	Val	Phe	Arg	Asp	Ser	Asp	His	Ala	Ala	Arg	Leu	
		35					40					45				
ttc	gca	ctg	gaa	gaa	cct	ggg	ttc	atc	tat	aca	agg	att	gga	aat	cct	192
Phe	Ala	Leu	Glu	Glu	Pro	Gly	Phe	Ile	Tyr	Thr	Arg	Ile	Gly	Asn	Pro	
	50					55					60					
acc	gtc	tca	gtt	ctt	gaa	gaa	aga	ata	gcc	gcc	ctg	gaa	gaa	ggg	gtg	240
Thr	Val	Ser	Val	Leu	Glu	Glu	Arg	Ile	Ala	Ala	Leu	Glu	Glu	Gly	Val	
65				70						75					80	
gga	gcc	tta	gcg	gtt	gcc	agt	gga	caa	gcc	gct	ata	act	tac	gcc	att	288
Gly	Ala	Leu	Ala	Val	Ala	Ser	Gly	Gln	Ala	Ala	Ile	Thr	Tyr	Ala	Ile	
			85					90						95		
ttg	aac	atc	gcg	ggc	cca	gga	gat	gag	atc	gtc	agc	ggg	agc	gcg	ctg	336
Leu	Asn	Ile	Ala	Gly	Pro	Gly	Asp	Glu	Ile	Val	Ser	Gly	Ser	Ala	Leu	
			100					105					110			
tat	ggg	gga	acg	tac	aat	ctg	ttc	aga	cac	act	ctc	tat	aaa	aaa	tcc	384
Tyr	Gly	Gly	Thr	Tyr	Asn	Leu	Phe	Arg	His	Thr	Leu	Tyr	Lys	Lys	Ser	
		115				120					125					
ggc	atc	atc	gtg	aag	ttt	gtg	gat	gag	aca	gat	cca	aag	aac	ata	gaa	432
Gly	Ile	Ile	Val	Lys	Phe	Val	Asp	Glu	Thr	Asp	Pro	Lys	Asn	Ile	Glu	
	130					135					140					
gag	gcc	atc	acc	gag	aaa	aca	aag	gcg	gtg	tac	ctt	gaa	act	atc	ggg	480
Glu	Ala	Ile	Thr	Glu	Lys	Thr	Lys	Ala	Val	Tyr	Leu	Glu	Thr	Ile	Gly	
145				150						155					160	
aat	ccc	ggt	ctc	aca	gtg	ccg	gac	ttt	gaa	gcg	ata	gcg	gag	atc	gct	528
Asn	Pro	Gly	Leu	Thr	Val	Pro	Asp	Phe	Glu	Ala	Ile	Ala	Glu	Ile	Ala	
			165						170					175		
cac	aga	cac	ggt	gtt	cct	ttg	ata	gtg	gac	aat	acg	gta	gct	ccg	tac	576
His	Arg	His	Gly	Val	Pro	Leu	Ile	Val	Asp	Asn	Thr	Val	Ala	Pro	Tyr	
			180					185				190				
ata	ttc	agg	ccc	ttc	gaa	cac	ggt	gcc	gac	atc	gtt	gtt	tat	tcg	gcc	624
Ile	Phe	Arg	Pro	Phe	Glu	His	Gly	Ala	Asp	Ile	Val	Val	Tyr</			

gaa gca gcc tac ata gca aaa tgt aga acc cag ctt ttg agg gac ctg 816
 Glu Ala Ala Tyr Ile Ala Lys Cys Arg Thr Gln Leu Leu Arg Asp Leu
 260 265 270
 gga agc tgt atg agc ccg ttc aac gcg ttt ctg ttc atc ctc gga ctt 864
 Gly Ser Cys Met Ser Pro Phe Asn Ala Phe Leu Phe Ile Leu Gly Leu
 275 280 285
 gaa acc ctc agc ttg agg atg aag aaa cac tgt gaa aac gca ctg aag 912
 Glu Thr Leu Ser Leu Arg Met Lys Lys His Cys Glu Asn Ala Leu Lys
 290 295 300
 atc gtt gaa ttt ctg aaa tcg cat ccc gcc gtg agc tgg gtc aac tat 960
 Ile Val Glu Phe Leu Lys Ser His Pro Ala Val Ser Trp Val Asn Tyr
 305 310 315 320
 ccg ata gct gaa ggc aat aaa acc aga gaa aat gcg ctg aaa tac ctc 1008
 Pro Ile Ala Glu Gly Asn Lys Thr Arg Glu Asn Ala Leu Lys Tyr Leu
 325 330 335
 aaa gaa gga tac ggt gcg att gta acg ttc ggt gtg aaa ggc gga aaa 1056
 Lys Glu Gly Tyr Gly Ala Ile Val Thr Phe Gly Val Lys Gly Gly Lys
 340 345 350
 gag gcg gga aag aag ttc ata gac agt ctc aca ctc att tcc cac ctc 1104
 Glu Ala Gly Lys Lys Phe Ile Asp Ser Leu Thr Leu Ile Ser His Leu
 355 360 365
 gcc aac att ggt gat gca aga act ctg gct att cat ccc gct tcg aca 1152
 Ala Asn Ile Gly Asp Ala Arg Thr Leu Ala Ile His Pro Ala Ser Thr
 370 375 380
 acc cat cag cag ctc acg gaa gaa gag cag ttg aaa acg ggt gtt act 1200
 Thr His Gln Gln Leu Thr Glu Glu Glu Gln Leu Lys Thr Gly Val Thr
 385 390 395 400
 ccg gat atg ata aga ttg tct gtt gga ata gaa gat gtg gaa gat atc 1248
 Pro Asp Met Ile Arg Leu Ser Val Gly Ile Glu Asp Val Glu Asp Ile
 405 410 415
 ata gcc gat ctg gat cag gct ctc aga aaa tct cag gag gga tga 1293
 Ile Ala Asp Leu Asp Gln Ala Leu Arg Lys Ser Gln Glu Gly
 420 425 430

<210> 30

<211> 430

<212> PRT

<213> Thermotoga maritima

<400> 30

Met Asp Trp Lys Lys Tyr Gly Tyr Asn Thr Arg Ala Leu His Ala Gly
1 5 10 15

Tyr Glu Pro Pro Glu Gln Ala Thr Gly Ser Arg Ala Val Pro Ile Tyr
20 25 30

Gln Thr Thr Ser Tyr Val Phe Arg Asp Ser Asp His Ala Ala Arg Leu

35		40		45											
Phe	Ala	Leu	Glu	Glu	Pro	Gly	Phe	Ile	Tyr	Thr	Arg	Ile	Gly	Asn	Pro
50						55					60				
Thr	Val	Ser	Val	Leu	Glu	Glu	Arg	Ile	Ala	Ala	Leu	Glu	Glu	Gly	Val
65				70					75						80
Gly	Ala	Leu	Ala	Val	Ala	Ser	Gly	Gln	Ala	Ala	Ile	Thr	Tyr	Ala	Ile
				85					90					95	
Leu	Asn	Ile	Ala	Gly	Pro	Gly	Asp	Glu	Ile	Val	Ser	Gly	Ser	Ala	Leu
			100					105					110		
Tyr	Gly	Gly	Thr	Tyr	Asn	Leu	Phe	Arg	His	Thr	Leu	Tyr	Lys	Lys	Ser
		115					120					125			
Gly	Ile	Ile	Val	Lys	Phe	Val	Asp	Glu	Thr	Asp	Pro	Lys	Asn	Ile	Glu
	130					135					140				
Glu	Ala	Ile	Thr	Glu	Lys	Thr	Lys	Ala	Val	Tyr	Leu	Glu	Thr	Ile	Gly
145					150					155					160
Asn	Pro	Gly	Leu	Thr	Val	Pro	Asp	Phe	Glu	Ala	Ile	Ala	Glu	Ile	Ala
				165					170					175	
His	Arg	His	Gly	Val	Pro	Leu	Ile	Val	Asp	Asn	Thr	Val	Ala	Pro	Tyr
			180					185					190		
Ile	Phe	Arg	Pro	Phe	Glu	His	Gly	Ala	Asp	Ile	Val	Val	Tyr	Ser	Ala
		195					200					205			
Thr	Lys	Phe	Ile	Gly	Gly	His	Gly	Thr	Ser	Ile	Gly	Gly	Leu	Ile	Val
	210					215					220				
Asp	Ser	Gly	Lys	Phe	Asp	Trp	Thr	Asn	Gly	Lys	Phe	Pro	Glu	Leu	Val
225					230					235					240
Glu	Pro	Asp	Pro	Ser	Tyr	His	Gly	Val	Ser	Tyr	Val	Glu	Thr	Phe	Lys
				245					250					255	
Glu	Ala	Ala	Tyr	Ile	Ala	Lys	Cys	Arg	Thr	Gln	Leu	Leu	Arg	Asp	Leu
			260					265					270		
Gly	Ser	Cys	Met	Ser	Pro	Phe	Asn	Ala	Phe	Leu	Phe	Ile	Leu	Gly	Leu
		275					280					285			
Glu	Thr	Leu	Ser	Leu	Arg	Met	Lys	Lys	His	Cys	Glu	Asn	Ala	Leu	Lys
	290					295					300				

Ile Val Glu Phe Leu Lys Ser His Pro Ala Val Ser Trp Val Asn Tyr
305 310 315 320

Pro Ile Ala Glu Gly Asn Lys Thr Arg Glu Asn Ala Leu Lys Tyr Leu
325 330 335

Lys Glu Gly Tyr Gly Ala Ile Val Thr Phe Gly Val Lys Gly Gly Lys
340 345 350

Glu Ala Gly Lys Lys Phe Ile Asp Ser Leu Thr Leu Ile Ser His Leu
355 360 365

Ala Asn Ile Gly Asp Ala Arg Thr Leu Ala Ile His Pro Ala Ser Thr
370 375 380

Thr His Gln Gln Leu Thr Glu Glu Glu Gln Leu Lys Thr Gly Val Thr
385 390 395 400

Pro Asp Met Ile Arg Leu Ser Val Gly Ile Glu Asp Val Glu Asp Ile
405 410 415

Ile Ala Asp Leu Asp Gln Ala Leu Arg Lys Ser Gln Glu Gly
420 425 430

<210> 31

<211> 1314

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(1314)

<223>

<400> 31

atg	gag	cta	att	aat	aat	aaa	agg	aga	gct	tcc	atg	act	cga	gaa	ttt	48
Met	Glu	Leu	Ile	Asn	Asn	Lys	Arg	Arg	Ala	Ser	Met	Thr	Arg	Glu	Phe	
1				5					10					15		

tct	ttt	gaa	act	tta	caa	tta	cat	gcg	gga	caa	agt	gtt	gat	cct	aca	96
Ser	Phe	Glu	Thr	Leu	Gln	Leu	His	Ala	Gly	Gln	Ser	Val	Asp	Pro	Thr	
			20					25					30			

aca	aaa	tcg	cgt	gca	gta	cca	atc	tat	cag	acg	act	tcc	tat	gtg	ttt	144
Thr	Lys	Ser	Arg	Ala	Val	Pro	Ile	Tyr	Gln	Thr	Thr	Ser	Tyr	Val	Phe	
		35					40					45				

aat	gat	gca	caa	gat	gct	gaa	gat	tct	ttt	gca	ctt	cgt	aca	ccc	ggc	192
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Asn 50	Asp	Ala	Gln	Asp	Ala	Glu 55	Asp	Ser	Phe	Ala	Leu 60	Arg	Thr	Pro	Gly	
aat 65	att Ile	tat Tyr	acg Thr	cgg Arg	atc Ile	act Thr	aat Asn	ccg Pro	act Thr	aca Thr	gcc Ala	gtt Val	ttt Phe	gaa Glu	gaa Glu 80	240
cgg Arg	atg Met	gcc Ala	gct Ala	ctt Leu 85	gaa Glu	ggg Gly	ggg Gly	gtc Val	ggg Gly	gca Ala	ctg Leu	gca Ala	aca Thr	gct Ala 95	tct Ser	288
ggg Gly	atg Met	gca Ala	gca Ala	gta Val 100	act Thr	tat Tyr	att Ile	gcc Ala 105	ttg Leu	gct Ala	ctt Leu	gct Ala	cat His 110	gca Ala	ggg Gly	336
gat Asp	cat His	att Ile 115	gtg Val	tca Ser	gca Ala	gcg Ala	aca Thr 120	gtt Val	tac Tyr	ggg Gly	ggc Gly	act Thr 125	ttt Phe	aat Asn	ctt Leu	384
ctt Leu 130	aag Lys	gaa Glu	act Thr	tta Leu	cct Pro	cgc Arg 135	tat Tyr	ggc Gly	att Ile	act Thr	aca Thr 140	agt Ser	ttt Phe	gtt Val	gat Asp	432
gtt Val 145	gct Ala	aat Asn	ttc Phe	gct Ala	gaa Glu 150	att Ile	gaa Glu	gcg Ala	gct Ala	att Ile 155	aca Thr	gac Asp	aag Lys	act Thr	aag Lys 160	480
ttt Phe	att Ile	atc Ile	gct Ala	gaa Glu 165	acg Thr	tta Leu	gga Gly	aat Asn	cct Pro 170	ctt Leu	gga Gly	aat Asn	atc Ile	gct Ala 175	gat Asp	528
ctt Leu	gaa Glu	aaa Lys	tta Leu 180	gct Ala	gag Glu	att Ile	gcc Ala	cat His 185	cga Arg	cat His	gct Ala	att Ile	ccc Pro 190	ttg Leu	gtt Val	576
att Ile	gat Asp	aat Asn 195	acc Thr	ttt Phe	ggg Gly	act Thr	cct Pro 200	tat Tyr	ttg Leu	ctt Leu	aat Asn	gtc Val 205	ttc Phe	tct Ser	tac Tyr	624
ggg Gly	gtt Val 210	gat Asp	att Ile	gct Ala	gtt Val	cat His 215	tct Ser	gcc Ala	act Thr	aaa Lys	ttt Phe 220	atc Ile	ggg Gly	gga Gly	cat His	672
ggg Gly 225	aca Thr	tct Ser	att Ile	ggc Gly	ggg Gly 230	gtc Val	att Ile	gtt Val	gat Asp	tct Ser 235	gga Gly	aac Asn	ttt Phe	gat Asp	tgg Trp 240	720
gaa Glu	aaa Lys	tct Ser	gga Gly	aaa Lys 245	ttc Phe	cca Pro	caa Gln	ttt Phe	gta Val 250	gaa Glu	cca Pro	gat Asp	cct Pro	tcc Ser 255	tat Tyr	768
cat His	gac Asp	att Ile	agt Ser	tat Tyr	aca Thr	cgt Arg	gat Asp	att Ile 265	gga Gly	aaa Lys	gca Ala	gct Ala	ttt Phe 270	gta Val	act Thr	816
gcg Ala	gtg Val	cgt Arg 275	acg Thr	caa Gln	ctg Leu	ctg Leu	cgt Arg 280	gat Asp	aca Thr	ggc Gly	gcc Ala	tgc Cys 285	ctt Leu	tca Ser	cct Pro	864
ttc Phe 290	aat Asn	gcc Ala	ttt Phe	ctt Leu	ttg Leu	cta Leu 295	caa Gln	ggg Gly	cta Leu	gaa Glu	acc Thr 300	tta Leu	tca Ser	ctt Leu	cgt Arg	912
gtt Val 305	gag Glu	cgt Arg	cat His	gtg Val	gaa Glu 310	aat Asn	gct Ala	aag Lys	aaa Lys	att Ile 315	gcg Ala	tac Tyr	tat Tyr	ctg Leu	gaa Glu 320	960

aat cat cct aaa gtc aca aaa gtt aat tat gct agt ttg cca tca agt 1008
 Asn His Pro Lys Val Thr Lys Val Asn Tyr Ala Ser Leu Pro Ser Ser
 325 330 335

 cct tat tat gac ttg gct caa aaa tac ttg cca aaa gga gct agt tct 1056
 Pro Tyr Tyr Asp Leu Ala Gln Lys Tyr Leu Pro Lys Gly Ala Ser Ser
 340 345 350

 atc ttt act ttt aat gtt gca ggc agt gcg aaa gcc gct cgc gag gtc 1104
 Ile Phe Thr Phe Asn Val Ala Gly Ser Ala Lys Ala Ala Arg Glu Val
 355 360 365

 att gac agt ctt gaa atc ttt tct gat ttg gcg aat gtt gct gat gcc 1152
 Ile Asp Ser Leu Glu Ile Phe Ser Asp Leu Ala Asn Val Ala Asp Ala
 370 375 380

 aaa tca cta gtt gtt cat ccg gca aca acc act cat ggt caa atg act 1200
 Lys Ser Leu Val Val His Pro Ala Thr Thr Thr His Gly Gln Met Thr
 385 390 395 400

 gaa gaa gat cta cga gct tgc ggt att gaa cct gag caa atc cgt gtt 1248
 Glu Glu Asp Leu Arg Ala Cys Gly Ile Glu Pro Glu Gln Ile Arg Val
 405 410 415

 tct att ggt ttg gaa aat gct gat gac tta atc gaa gat ttg cgc cta 1296
 Ser Ile Gly Leu Glu Asn Ala Asp Asp Leu Ile Glu Asp Leu Arg Leu
 420 425 430

 gca ctt gaa aaa ata taa 1314
 Ala Leu Glu Lys Ile
 435

<210> 32

<211> 437

<212> PRT

<213> Streptococcus mutans

<400> 32

Met Glu Leu Ile Asn Asn Lys Arg Arg Ala Ser Met Thr Arg Glu Phe
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 Ser Phe Glu Thr Leu Gln Leu His Ala Gly Gln Ser Val Asp Pro Thr
 20 25 30

 Thr Lys Ser Arg Ala Val Pro Ile Tyr Gln Thr Thr Ser Tyr Val Phe
 35 40 45

 Asn Asp Ala Gln Asp Ala Glu Asp Ser Phe Ala Leu Arg Thr Pro Gly
 50 55 60

 Asn Ile Tyr Thr Arg Ile Thr Asn Pro Thr Thr Ala Val Phe Glu Glu
 65 70 75 80

 Arg Met Ala Ala Leu Glu Gly Gly Val Gly Ala Leu Ala Thr Ala Ser
 85 90 95

Gly Met Ala Ala Val Thr Tyr Ile Ala Leu Ala Leu Ala His Ala Gly
 100 105 110
 Asp His Ile Val Ser Ala Ala Thr Val Tyr Gly Gly Thr Phe Asn Leu
 115 120 125
 Leu Lys Glu Thr Leu Pro Arg Tyr Gly Ile Thr Thr Ser Phe Val Asp
 130 135 140
 Val Ala Asn Phe Ala Glu Ile Glu Ala Ala Ile Thr Asp Lys Thr Lys
 145 150 155 160
 Phe Ile Ile Ala Glu Thr Leu Gly Asn Pro Leu Gly Asn Ile Ala Asp
 165 170 175
 Leu Glu Lys Leu Ala Glu Ile Ala His Arg His Ala Ile Pro Leu Val
 180 185 190
 Ile Asp Asn Thr Phe Gly Thr Pro Tyr Leu Leu Asn Val Phe Ser Tyr
 195 200 205
 Gly Val Asp Ile Ala Val His Ser Ala Thr Lys Phe Ile Gly Gly His
 210 215 220
 Gly Thr Ser Ile Gly Gly Val Ile Val Asp Ser Gly Asn Phe Asp Trp
 225 230 235 240
 Glu Lys Ser Gly Lys Phe Pro Gln Phe Val Glu Pro Asp Pro Ser Tyr
 245 250 255
 His Asp Ile Ser Tyr Thr Arg Asp Ile Gly Lys Ala Ala Phe Val Thr
 260 265 270
 Ala Val Arg Thr Gln Leu Leu Arg Asp Thr Gly Ala Cys Leu Ser Pro
 275 280 285
 Phe Asn Ala Phe Leu Leu Leu Gln Gly Leu Glu Thr Leu Ser Leu Arg
 290 295 300
 Val Glu Arg His Val Glu Asn Ala Lys Lys Ile Ala Tyr Tyr Leu Glu
 305 310 315 320
 Asn His Pro Lys Val Thr Lys Val Asn Tyr Ala Ser Leu Pro Ser Ser
 325 330 335
 Pro Tyr Tyr Asp Leu Ala Gln Lys Tyr Leu Pro Lys Gly Ala Ser Ser
 340 345 350
 Ile Phe Thr Phe Asn Val Ala Gly Ser Ala Lys Ala Ala Arg Glu Val

355 360 365
 Ile Asp Ser Leu Glu Ile Phe Ser Asp Leu Ala Asn Val Ala Asp Ala
 370 375 380
 Lys Ser Leu Val Val His Pro Ala Thr Thr Thr His Gly Gln Met Thr
 385 390 395 400
 Glu Glu Asp Leu Arg Ala Cys Gly Ile Glu Pro Glu Gln Ile Arg Val
 405 410 415
 Ser Ile Gly Leu Glu Asn Ala Asp Asp Leu Ile Glu Asp Leu Arg Leu
 420 425 430
 Ala Leu Glu Lys Ile
 435

<210> 33

<211> 1431

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (1)..(1431)

<223>

<400> 33

ttg aag cgc cgc acg ccg gtg ata gga tgg ccg cca ctt tca cct ttc	48
Leu Lys Arg Arg Thr Pro Val Ile Gly Trp Pro Pro Leu Ser Pro Phe	
1 5 10 15	
gcg agg ccg tcc gtg gcc ccg ccg ccc agc atg tcc gcg aac cgt ttc	96
Ala Arg Pro Ser Val Ala Pro Pro Pro Ser Met Ser Ala Asn Arg Phe	
20 25 30	
gac acg ctt gcg ctg cac gcc ggc gct gct ccc gac ccg acc acc ggc	144
Asp Thr Leu Ala Leu His Ala Gly Ala Ala Pro Asp Pro Thr Thr Gly	
35 40 45	
gcg cgc gcc acg ccg att tac cag act acc tcg ttt tcg ttc cgc gat	192
Ala Arg Ala Thr Pro Ile Tyr Gln Thr Thr Ser Phe Ser Phe Arg Asp	
50 55 60	
tcc gac cac gcc gcg gcg ctc ttc aat atg gag cgc gcc ggt cat gtt	240
Ser Asp His Ala Ala Ala Leu Phe Asn Met Glu Arg Ala Gly His Val	
65 70 75 80	
tat tcg cgc att tcg aac ccg acc gtg gcc gtg ttc gag gaa cgc gtg	288
Tyr Ser Arg Ile Ser Asn Pro Thr Val Ala Val Phe Glu Glu Arg Val	
85 90 95	

gcc gcg ctg gaa aac ggc gcg ggc gcg atc ggc acg gca agc ggc cag Ala Ala Leu Glu Asn Gly Ala Gly Ala Ile Gly Thr Ala Ser Gly Gln 100 105 110	336
gcg gcc ctg cat ctg gcc att gcc acg ctg atg ggc gcg ggt tcg cat Ala Ala Leu His Leu Ala Ile Ala Thr Leu Met Gly Ala Gly Ser His 115 120 125	384
atc gtc gcc tcc agc gcg ctg tac ggc ggc tcg cac aat ctg ctg cac Ile Val Ala Ser Ser Ala Leu Tyr Gly Gly Ser His Asn Leu Leu His 130 135 140	432
tac acg ttg cgg cgc ttc ggc atc gag acg act ttc gtc aaa ccc ggc Tyr Thr Leu Arg Arg Phe Gly Ile Glu Thr Thr Phe Val Lys Pro Gly 145 150 155 160	480
gac ctg gac gcg tgg cgc gcc gcg ctg cgc cca aac acg cgg ctg ctg Asp Leu Asp Ala Trp Arg Ala Ala Leu Arg Pro Asn Thr Arg Leu Leu 165 170 175	528
ttc ggc gag acg ctc ggc aat ccg ggg ctc gac gtg ctc gat atc gcc Phe Gly Glu Thr Leu Gly Asn Pro Gly Leu Asp Val Leu Asp Ile Ala 180 185 190	576
gcc gtc gcg cag atc gcg cat gag cac cgc gtg ccg ctg ctg gtc gac Ala Val Ala Gln Ile Ala His Glu His Arg Val Pro Leu Leu Val Asp 195 200 205	624
tcg acc ttc acc aca cct tac ctg ctc aaa ccg ttc gaa cat ggc gcg Ser Thr Phe Thr Thr Pro Tyr Leu Leu Lys Pro Phe Glu His Gly Ala 210 215 220	672
gac ttc gtc tat cac tcg gcc acc aaa ttc ctc ggc ggc cac ggc acg Asp Phe Val Tyr His Ser Ala Thr Lys Phe Leu Gly Gly His Gly Thr 225 230 235 240	720
acg atc ggc ggc gtg ctg gtg gac ggc ggc acg ttc gac ttc gac gcc Thr Ile Gly Gly Val Leu Val Asp Gly Gly Thr Phe Asp Phe Asp Ala 245 250 255	768
tcg ggg cgc ttc ccc gaa ttc acc gaa cct tac gac ggc ttt cac ggc Ser Gly Arg Phe Pro Glu Phe Thr Glu Pro Tyr Asp Gly Phe His Gly 260 265 270	816
atg gtg ttc gcc gag gag agc acc gtc gcg ccg ttt ctg ctg cga gca Met Val Phe Ala Glu Glu Ser Thr Val Ala Pro Phe Leu Leu Arg Ala 275 280 285	864
cgc cgc gag ggg ctg cgc gac ttc ggc gca tgc ctg cat ccg caa gcc Arg Arg Glu Gly Leu Arg Asp Phe Gly Ala Cys Leu His Pro Gln Ala 290 295 300	912
gca tgg caa ctg ctg caa ggc atc gag acg ctg ccg ttg cga atg gaa Ala Trp Gln Leu Leu Gln Gly Ile Glu Thr Leu Pro Leu Arg Met Glu 305 310 315 320	960
cgg cac gtt gcc aac acg cgc cgg gtg gtc gag ttc ctc gcc ggt cac Arg His Val Ala Asn Thr Arg Arg Val Val Glu Phe Leu Ala Gly His 325 330 335	1008
gcc gcg gtc ggg gcc gtc gcc tat ccg gaa ctg ccc acg cac ccc gac Ala Ala Val Gly Ala Val Ala Tyr Pro Glu Leu Pro Thr His Pro Asp 340 345 350	1056
cac gcg ctc gcg aag cgg ctg ctg ccg cgc ggc gcc ggt gcc gtg ttc His Ala Leu Ala Lys Arg Leu Leu Pro Arg Gly Ala Gly Ala Val Phe 1104	

355	360	365	
agc ttc gat ctg cgc ggc gac cgc gcc gcc gga cgc agc ttt atc gaa Ser Phe Asp Leu Arg Gly Asp Arg Ala Ala Gly Arg Ser Phe Ile Glu 370 375 380			1152
gcg ctc tcg ctg ttc tcg cat ctc gcg aac gtg ggc gac gcg cgc tcg Ala Leu Ser Leu Phe Ser His Leu Ala Asn Val Gly Asp Ala Arg Ser 385 390 395 400			1200
ctc gtg atc cat ccc gcc tcg acc acc cac ttt cgc atg gac gcc gct Leu Val Ile His Pro Ala Ser Thr Thr His Phe Arg Met Asp Ala Ala 405 410 415			1248
gcc ctt gcc gcg gcc ggt atc gcc gaa ggc acg atc cgc ctc tcg atc Ala Leu Ala Ala Ala Gly Ile Ala Glu Gly Thr Ile Arg Leu Ser Ile 420 425 430			1296
ggc ctc gaa gat ccc gac gat ctg atc gac gat ctc aag cgc gcg cta Gly Leu Glu Asp Pro Asp Asp Leu Ile Asp Asp Leu Lys Arg Ala Leu 435 440 445			1344
aag gcc gca cag aaa gcg ggc agt tcg agc gca gcg cac ggc ggc gca Lys Ala Ala Gln Lys Ala Gly Ser Ser Ser Ala Ala His Gly Gly Ala 450 455 460			1392
tcc ggc agt gcc gcc caa ccc cgc ccg gag tcc gca tga Ser Gly Ser Ala Ala Gln Pro Arg Pro Glu Ser Ala 465 470 475			1431

<210> 34

<211> 476

<212> PRT

<213> Burkholderia cepacia

<400> 34

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Ala Arg Pro Ser Val Ala Pro Pro Pro Ser Met Ser Ala Asn Arg Phe 20 25 30
Asp Thr Leu Ala Leu His Ala Gly Ala Ala Pro Asp Pro Thr Thr Gly 35 40 45
Ala Arg Ala Thr Pro Ile Tyr Gln Thr Thr Ser Phe Ser Phe Arg Asp 50 55 60
Ser Asp His Ala Ala Ala Leu Phe Asn Met Glu Arg Ala Gly His Val 65 70 75 80
Tyr Ser Arg Ile Ser Asn Pro Thr Val Ala Val Phe Glu Glu Arg Val 85 90 95

Ala Ala Leu Glu Asn Gly Ala Gly Ala Ile Gly Thr Ala Ser Gly Gln
 100 105 110
 Ala Ala Leu His Leu Ala Ile Ala Thr Leu Met Gly Ala Gly Ser His
 115 120 125
 Ile Val Ala Ser Ser Ala Leu Tyr Gly Gly Ser His Asn Leu Leu His
 130 135 140
 Tyr Thr Leu Arg Arg Phe Gly Ile Glu Thr Thr Phe Val Lys Pro Gly
 145 150 155 160
 Asp Leu Asp Ala Trp Arg Ala Ala Leu Arg Pro Asn Thr Arg Leu Leu
 165 170 175
 Phe Gly Glu Thr Leu Gly Asn Pro Gly Leu Asp Val Leu Asp Ile Ala
 180 185 190
 Ala Val Ala Gln Ile Ala His Glu His Arg Val Pro Leu Leu Val Asp
 195 200 205
 Ser Thr Phe Thr Thr Pro Tyr Leu Leu Lys Pro Phe Glu His Gly Ala
 210 215 220
 Asp Phe Val Tyr His Ser Ala Thr Lys Phe Leu Gly Gly His Gly Thr
 225 230 235 240
 Thr Ile Gly Gly Val Leu Val Asp Gly Gly Thr Phe Asp Phe Asp Ala
 245 250 255
 Ser Gly Arg Phe Pro Glu Phe Thr Glu Pro Tyr Asp Gly Phe His Gly
 260 265 270
 Met Val Phe Ala Glu Glu Ser Thr Val Ala Pro Phe Leu Leu Arg Ala
 275 280 285
 Arg Arg Glu Gly Leu Arg Asp Phe Gly Ala Cys Leu His Pro Gln Ala
 290 295 300
 Ala Trp Gln Leu Leu Gln Gly Ile Glu Thr Leu Pro Leu Arg Met Glu
 305 310 315 320
 Arg His Val Ala Asn Thr Arg Arg Val Val Glu Phe Leu Ala Gly His
 325 330 335
 Ala Ala Val Gly Ala Val Ala Tyr Pro Glu Leu Pro Thr His Pro Asp
 340 345 350
 His Ala Leu Ala Lys Arg Leu Leu Pro Arg Gly Ala Gly Ala Val Phe
 355 360 365

Ser Phe Asp Leu Arg Gly Asp Arg Ala Ala Gly Arg Ser Phe Ile Glu
370 375 380

Ala Leu Ser Leu Phe Ser His Leu Ala Asn Val Gly Asp Ala Arg Ser
385 390 395 400

Leu Val Ile His Pro Ala Ser Thr Thr His Phe Arg Met Asp Ala Ala
405 410 415

Ala Leu Ala Ala Ala Gly Ile Ala Glu Gly Thr Ile Arg Leu Ser Ile
420 425 430

Gly Leu Glu Asp Pro Asp Asp Leu Ile Asp Asp Leu Lys Arg Ala Leu
435 440 445

Lys Ala Ala Gln Lys Ala Gly Ser Ser Ser Ala Ala His Gly Gly Ala
450 455 460

Ser Gly Ser Ala Ala Gln Pro Arg Pro Glu Ser Ala
465 470 475

<210> 35

<211> 1722

<212> DNA

<213> Deinococcus radiodurans

<220>

<221> CDS

<222> (1)..(1722)

<223>

<400> 35	
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Val Ala Phe Pro Cys Gly Gln Ala Gly Asn Lys Ile Thr Arg Pro Gly	
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caa tgt gtc aac ggg ggc agg gca cgc tca gcc ccg tct aag ttt cgc	96
Gln Cys Val Asn Gly Gly Arg Ala Arg Ser Ala Pro Ser Lys Phe Arg	
20 25 30	
ctt gac ccc tta ccc gcc tcc gcg cta ctt ttt gag gag ctc ccg cag	144
Leu Asp Pro Leu Pro Ala Ser Ala Leu Leu Phe Glu Glu Leu Pro Gln	
35 40 45	
cag gag cca ccc act tca gag cgc ccg aga gac ctg gct cga cga cgg	192
Gln Glu Pro Pro Thr Ser Glu Arg Pro Arg Asp Leu Ala Arg Arg Arg	
50 55 60	
cgc ggc aac cgg acc cca tca cgt cac ggt gcc aag gcc agc ccc ctg	240

Arg 65	Gly	Asn	Arg	Thr	Pro 70	Ser	Arg	His	Gly	Ala 75	Lys	Ala	Ser	Pro	Leu 80	
ggc Gly	gtg Val	tca Ser	acg Thr	atg Met	agc Ser	cgc Arg	cgg Arg	gcg Ala	gga Gly	cca Pro	agc Ser	ggg Gly	aag Lys	gcc Ala	acg Thr	288
cgg Arg	atg Met	acg Thr	ata Ile	ttc Phe	aag Lys	tgt Cys	ccc Pro	ttc Phe	tcg Ser	att Ile	cac His	agc Ser	agg Arg	cag Gln	ggg Gly	336
gag Glu	tgc Cys	cgt Arg	gac Asp	tgg Trp	cgc Arg	ccc Pro	cga Arg	acc Thr	tgc Cys	ttc Phe	ccc Pro	cga Arg	gga Gly	gcc Ala	gcc Ala	384
acc Thr	atg Met	acc Thr	gat Asp	acc Thr	aaa Lys	cag Gln	ccg Pro	cag Gln	cct Pro	ctg Leu	cac His	ttc Phe	gag Glu	acc Thr	ttg Leu	432
cag Gln	gtg Val	cac His	gcc Ala	gga Gly	caa Gln	cgc Arg	ccc Pro	gac Asp	ccc Pro	gtg Val	acc Thr	gga Gly	gcg Ala	cag Gln	caa Gln	480
acg Thr	ccc Pro	atc Ile	tac Tyr	gcc Ala	acc Thr	aac Asn	tcc Ser	tac Tyr	gtg Val	ttc Phe	gag Glu	tcg Ser	ccc Pro	gag Glu	cac His	528
gcc Ala	gcc Ala	gac Asp	ctc Leu	ttc Phe	ggg Gly	ctg Leu	cgg Arg	caa Gln	ttc Phe	ggc Gly	aac Asn	atc Ile	tac Tyr	agc Ser	cgc Arg	576
atc Ile	atg Met	aac Asn	ccc Pro	acc Thr	aac Asn	gac Asp	gtg Val	ttc Phe	gag Glu	cag Gln	cgg Arg	gtg Val	gcc Ala	gcc Ala	ctc Leu	624
gaa Glu	ggg Gly	ggc Gly	gtg Val	ggg Gly	gcg Ala	ctg Leu	tcg Ser	gtg Val	tcg Ser	agc Ser	ggg Gly	cac His	gcg Ala	ggg Gly	cag Gln	672
ctc Leu	gtg Val	aca Thr	ttg Leu	ctc Leu	acg Thr	ctg Leu	gcg Ala	cag Gln	gcg Ala	gga Gly	gac Asp	aac Asn	atc Ile	gtc Val	tcg Ser	720
tcg Ser	ccc Pro	aac Asn	ctg Leu	tac Tyr	ggc Gly	ggc Gly	acc Thr	gtc Val	aac Asn	cag Gln	ttc Phe	cgc Arg	gtc Val	acg Thr	ctc Leu	768
aag Lys	cgg Arg	ctc Leu	ggc Gly	atc Ile	gag Glu	gtg Val	cgg Arg	ttt Phe	acc Thr	agc Ser	aaa Lys	gac Asp	gag Glu	cgc Arg	ccc Pro	816
gag Glu	gaa Glu	ttc Phe	gcc Ala	gcg Ala	ctg Leu	atc Ile	gac Asp	gag Glu	cgc Arg	acg Thr	cgg Arg	gcc Ala	gta Val	tat Tyr	ctg Leu	864
gaa Glu	acc Thr	atc Ile	ggc Gly	aac Asn	ccg Pro	gcg Ala	ctg Leu	aac Asn	att Ile	ccc Pro	gat Asp	ttc Phe	gag Glu	ggc Gly	gtg Val	912
gcg Ala	aaa Lys	gtc Val	gcg Ala	cac His	gag Glu	cac His	ggc Gly	gtc Val	gcg Ala	gtg Val	gtc Val	gtg Val	gac Asp	aac Asn	acc Thr	960
ttc Phe	ggg Gly	gcc Ala	ggc Gly	gga Gly	tac Tyr	tac Tyr	tgc Cys	cag Gln	ccg Pro	ctg Leu	cgg Arg	cac His	ggc Gly	gcc Ala	aac Asn	1008

atc gtg ctg cac tcg gcg agc aag tgg atc ggc ggg cac ggc aac ggc Ile Val Leu His Ser Ala Ser Lys Trp Ile Gly Gly His Gly Asn Gly 340 345 350	1056
atc ggc ggg gtc atc gtg gac ggc ggg aac ttc gac tgg ggc agc ggg Ile Gly Gly Val Ile Val Asp Gly Gly Asn Phe Asp Trp Gly Ser Gly 355 360 365	1104
cgg tat ccg ctg atg acc gag ccc tcg ccg agt tat cac ggg ctg aag Arg Tyr Pro Leu Met Thr Glu Pro Ser Pro Ser Tyr His Gly Leu Lys 370 375 380	1152
ttc tgg gag acg ttc ggg gaa ggc aac ggg ctg ggg ctg ccg aac atc Phe Trp Glu Thr Phe Gly Glu Gly Asn Gly Leu Gly Leu Pro Asn Ile 385 390 395 400	1200
gcc ttc atc acc cgc gcc cgc acc gag ggg ctg cgc gac ctg gga acg Ala Phe Ile Thr Arg Ala Arg Thr Glu Gly Leu Arg Asp Leu Gly Thr 405 410 415	1248
acc ctg gcg ccg cag cag gcg tgg cag ttt ctg caa ggc ctt gaa acc Thr Leu Ala Pro Gln Gln Ala Trp Gln Phe Leu Gln Gly Leu Glu Thr 420 425 430	1296
ctg agc ctg cgc gcc gag cgc cac gcc gag aac acc ctg gcg ctg gcg Leu Ser Leu Arg Ala Glu Arg His Ala Glu Asn Thr Leu Ala Leu Ala 435 440 445	1344
cac tgg ctc atc agc cac ccg gac gtg aag cag gtc act tac ccc ggc His Trp Leu Ile Ser His Pro Asp Val Lys Gln Val Thr Tyr Pro Gly 450 455 460	1392
ctg agc aac cac ccc cac tac gac cgg gcg cag acc tac ttg ccg cgc Leu Ser Asn His Pro His Tyr Asp Arg Ala Gln Thr Tyr Leu Pro Arg 465 470 475 480	1440
ggg gcg ggc gcg gtg ctc acc ttc gag ctg cgc ggg ggc cgg gcg gcg Gly Ala Gly Ala Val Leu Thr Phe Glu Leu Arg Gly Gly Arg Ala Ala 485 490 495	1488
ggc gaa gcg ttt att cgc tcg gtc aag ctc gcg cag cac gtc gcc aac Gly Glu Ala Phe Ile Arg Ser Val Lys Leu Ala Gln His Val Ala Asn 500 505 510	1536
gtg ggc gac acc cgc acg ctg gtc att cat ccg gcg agc acc acc cac Val Gly Asp Thr Arg Thr Leu Val Ile His Pro Ala Ser Thr Thr His 515 520 525	1584
agc cag ctc gac gag gtg acg cag acg aac gcc ggg gtc acg ccg ggc Ser Gln Leu Asp Glu Val Thr Gln Thr Asn Ala Gly Val Thr Pro Gly 530 535 540	1632
ctc atc cgg gtg tcg gtg ggc atc gag cac gta gac gac atc cgc gag Leu Ile Arg Val Ser Val Gly Ile Glu His Val Asp Asp Ile Arg Glu 545 550 555 560	1680
gac ttc gcg cag gcc ctg gcg agc gct ggg gag cgg gcg tga Asp Phe Ala Gln Ala Leu Ala Ser Ala Gly Glu Arg Ala 565 570	1722

<210> 36

<211> 573

<212> PRT

<213> Deinococcus radiodurans

<400> 36

Val Ala Phe Pro Cys Gly Gln Ala Gly Asn Lys Ile Thr Arg Pro Gly
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 Gln Cys Val Asn Gly Gly Arg Ala Arg Ser Ala Pro Ser Lys Phe Arg
 20 25 30
 Leu Asp Pro Leu Pro Ala Ser Ala Leu Leu Phe Glu Glu Leu Pro Gln
 35 40 45
 Gln Glu Pro Pro Thr Ser Glu Arg Pro Arg Asp Leu Ala Arg Arg Arg
 50 55 60
 Arg Gly Asn Arg Thr Pro Ser Arg His Gly Ala Lys Ala Ser Pro Leu
 65 70 75 80
 Gly Val Ser Thr Met Ser Arg Arg Ala Gly Pro Ser Gly Lys Ala Thr
 85 90 95
 Arg Met Thr Ile Phe Lys Cys Pro Phe Ser Ile His Ser Arg Gln Gly
 100 105 110
 Glu Cys Arg Asp Trp Arg Pro Arg Thr Cys Phe Pro Arg Gly Ala Ala
 115 120 125
 Thr Met Thr Asp Thr Lys Gln Pro Gln Pro Leu His Phe Glu Thr Leu
 130 135 140
 Gln Val His Ala Gly Gln Arg Pro Asp Pro Val Thr Gly Ala Gln Gln
 145 150 155 160
 Thr Pro Ile Tyr Ala Thr Asn Ser Tyr Val Phe Glu Ser Pro Glu His
 165 170 175
 Ala Ala Asp Leu Phe Gly Leu Arg Gln Phe Gly Asn Ile Tyr Ser Arg
 180 185 190
 Ile Met Asn Pro Thr Asn Asp Val Phe Glu Gln Arg Val Ala Ala Leu
 195 200 205
 Glu Gly Gly Val Gly Ala Leu Ser Val Ser Ser Gly His Ala Gly Gln
 210 215 220
 Leu Val Thr Leu Leu Thr Leu Ala Gln Ala Gly Asp Asn Ile Val Ser
 225 230 235 240
 Ser Pro Asn Leu Tyr Gly Gly Thr Val Asn Gln Phe Arg Val Thr Leu

245					250					255					
Lys	Arg	Leu	Gly 260	Ile	Glu	Val	Arg	Phe 265	Thr	Ser	Lys	Asp	Glu 270	Arg	Pro
Glu	Glu	Phe 275	Ala	Ala	Leu	Ile	Asp 280	Glu	Arg	Thr	Arg	Ala 285	Val	Tyr	Leu
Glu	Thr 290	Ile	Gly	Asn	Pro	Ala 295	Leu	Asn	Ile	Pro	Asp 300	Phe	Glu	Gly	Val
Ala 305	Lys	Val	Ala	His 310	Glu	His	Gly	Val	Ala 315	Val	Val	Val	Asp	Asn	Thr 320
Phe	Gly	Ala	Gly	Gly 325	Tyr	Tyr	Cys	Gln	Pro 330	Leu	Arg	His	Gly	Ala 335	Asn
Ile	Val	Leu	His 340	Ser	Ala	Ser	Lys	Trp 345	Ile	Gly	Gly	His	Gly 350	Asn	Gly
Ile	Gly	Gly 355	Val	Ile	Val	Asp	Gly 360	Gly	Asn	Phe	Asp	Trp 365	Gly	Ser	Gly
Arg	Tyr 370	Pro	Leu	Met	Thr	Glu 375	Pro	Ser	Pro	Ser	Tyr 380	His	Gly	Leu	Lys
Phe 385	Trp	Glu	Thr	Phe	Gly 390	Glu	Gly	Asn	Gly	Leu	Gly 395	Leu	Pro	Asn	Ile 400
Ala	Phe	Ile	Thr	Arg 405	Ala	Arg	Thr	Glu	Gly 410	Leu	Arg	Asp	Leu	Gly 415	Thr
Thr	Leu	Ala	Pro 420	Gln	Gln	Ala	Trp	Gln 425	Phe	Leu	Gln	Gly	Leu 430	Glu	Thr
Leu	Ser	Leu 435	Arg	Ala	Glu	Arg	His 440	Ala	Glu	Asn	Thr	Leu	Ala 445	Leu	Ala
His 450	Trp	Leu	Ile	Ser	His	Pro 455	Asp	Val	Lys	Gln	Val 460	Thr	Tyr	Pro	Gly
Leu 465	Ser	Asn	His	Pro	His 470	Tyr	Asp	Arg	Ala	Gln 475	Thr	Tyr	Leu	Pro	Arg 480
Gly	Ala	Gly	Ala	Val 485	Leu	Thr	Phe	Glu	Leu 490	Arg	Gly	Gly	Arg	Ala 495	Ala
Gly	Glu	Ala	Phe 500	Ile	Arg	Ser	Val	Lys 505	Leu	Ala	Gln	His	Val 510	Ala	Asn

Val Gly Asp Thr Arg Thr Leu Val Ile His Pro Ala Ser Thr Thr His
515 520 525

Ser Gln Leu Asp Glu Val Thr Gln Thr Asn Ala Gly Val Thr Pro Gly
530 535 540

Leu Ile Arg Val Ser Val Gly Ile Glu His Val Asp Asp Ile Arg Glu
545 550 555 560

Asp Phe Ala Gln Ala Leu Ala Ser Ala Gly Glu Arg Ala
565 570

<210> 37

<211> 1284

<212> DNA

<213> Rhodobacter capsulatus

<220>

<221> CDS

<222> (1)..(1284)

<223>

<400> 37

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1 5 10 15	

ccc gat ccc gcg acg ggc gcg cgg cag gtg ccg att tac cag acc acc	96
Pro Asp Pro Ala Thr Gly Ala Arg Gln Val Pro Ile Tyr Gln Thr Thr	
20 25 30	

tcc tat gtc ttc aag gac gcc gac cat gcc gcg cgc ctg ttc ggg ctg	144
Ser Tyr Val Phe Lys Asp Ala Asp His Ala Ala Arg Leu Phe Gly Leu	
35 40 45	

cag gag gtg ggc tat atc tat tcc cgc ctg acc aac ccg acc gtt tcg	192
Gln Glu Val Gly Tyr Ile Tyr Ser Arg Leu Thr Asn Pro Thr Val Ser	
50 55 60	

gca ctg gcc gcc cgc gtt gcg gcg ctt gaa ggc ggc gtg ggc gcg gtc	240
Ala Leu Ala Ala Arg Val Ala Ala Leu Glu Gly Gly Val Gly Ala Val	
65 70 75 80	

tgc tgc tcg tcc ggc cat gcg gcg cag atc atg gcg ctg ttt ccg ctg	288
Cys Cys Ser Ser Gly His Ala Ala Gln Ile Met Ala Leu Phe Pro Leu	
85 90 95	

atg ggg ccg ggg ctg aac atc gtc gcc tcg acc ccg ctt tac ggc ggc	336
Met Gly Pro Gly Leu Asn Ile Val Ala Ser Thr Arg Leu Tyr Gly Gly	
100 105 110	

acg atc acc cag ttc agc cag acc atc aaa cgc ttc ggc tgg tcc tgc	384
Thr Ile Thr Gln Phe Ser Gln Thr Ile Lys Arg Phe Gly Trp Ser Cys	

115				120				125								
acc	ttt	gtc	gat	ttc	gac	gat	ctg	gcg	gcg	ctc	gag	gcc	gcg	gtg	gat	432
Thr	Phe	Val	Asp	Phe	Asp	Asp	Leu	Ala	Ala	Leu	Glu	Ala	Ala	Val	Asp	
	130					135					140					
gac	aac	acc	cgg	gcg	atc	ttt	tgc	gaa	tcg	atc	tcg	aac	ccg	ggc	ggc	480
Asp	Asn	Thr	Arg	Ala	Ile	Phe	Cys	Glu	Ser	Ile	Ser	Asn	Pro	Gly	Gly	
145					150					155					160	
tac	atc	acc	gac	ctg	ccc	gcc	gtc	gcg	gcg	gtg	gcg	aac	aag	gtc	ggc	528
Tyr	Ile	Thr	Asp	Leu	Pro	Ala	Val	Ala	Ala	Val	Ala	Asn	Lys	Val	Gly	
				165						170				175		
ctg	ccg	ctc	att	gtc	gac	aac	acg	ctg	gcc	tcg	cct	tat	ctc	tgc	cgc	576
Leu	Pro	Leu	Ile	Val	Asp	Asn	Thr	Leu	Ala	Ser	Pro	Tyr	Leu	Cys	Arg	
			180					185					190			
ccg	atc	gag	cat	ggc	gcg	acg	ctg	gtt	gtc	cat	tcc	gcc	acg	aaa	tac	624
Pro	Ile	Glu	His	Gly	Ala	Thr	Leu	Val	Val	His	Ser	Ala	Thr	Lys	Tyr	
	195						200					205				
ctg	acc	ggc	aac	ggc	acg	gtg	acg	ggc	ggg	gtg	atc	gtc	gat	tcg	ggc	672
Leu	Thr	Gly	Asn	Gly	Thr	Val	Thr	Gly	Gly	Val	Ile	Val	Asp	Ser	Gly	
	210					215					220					
aag	ttc	gac	tgg	tcg	gcc	tcg	ggc	aag	ttc	ccc	agc	ctt	tcg	gcg	ccc	720
Lys	Phe	Asp	Trp	Ser	Ala	Ser	Gly	Lys	Phe	Pro	Ser	Leu	Ser	Ala	Pro	
225					230					235					240	
gaa	ccc	gcc	tat	cac	ggg	ctg	aag	ttc	cac	gag	gca	ctc	ggc	ccg	atg	768
Glu	Pro	Ala	Tyr	His	Gly	Leu	Lys	Phe	His	Glu	Ala	Leu	Gly	Pro	Met	
				245					250					255		
gcc	ttc	acc	ttc	cat	tcg	atc	gcc	gtc	ggg	ctg	cgc	gat	ctg	ggc	atg	816
Ala	Phe	Thr	Phe	His	Ser	Ile	Ala	Val	Gly	Leu	Arg	Asp	Leu	Gly	Met	
			260					265					270			
acg	atg	aac	ccg	cag	ggc	gcg	cat	tac	acg	ctg	atg	ggg	atc	gag	acg	864
Thr	Met	Asn	Pro	Gln	Gly	Ala	His	Tyr	Thr	Leu	Met	Gly	Ile	Glu	Thr	
	275						280					285				
ctc	agc	ctg	cgc	atg	gac	aag	cac	gtc	gcc	aat	gcg	aag	gcg	gtg	gcg	912
Leu	Ser	Leu	Arg	Met	Asp	Lys	His	Val	Ala	Asn	Ala	Lys	Ala	Val	Ala	
	290					295					300					
gaa	tgg	ctg	gcc	aaa	gac	ccg	cgc	atc	gac	ttc	gtc	acc	tgg	gcc	ggg	960
Glu	Trp	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Asp	Phe	Val	Thr	Trp	Ala	Gly	
305					310					315					320	
ctg	ccc	tcc	tcg	ccc	tgg	cac	gaa	cgc	gcc	gag	cgg	ctt	tgc	ccg	aag	1008
Leu	Pro	Ser	Ser	Pro	Trp	His	Glu	Arg	Ala	Glu	Arg	Leu	Cys	Pro	Lys	
				325					330					335		
ggg	gcg	ggg	gcg	ctt	ttc	acc	gtc	gcg	gtc	aag	ggc	ggc	tat	gag	gcc	1056
Gly	Ala	Gly	Ala	Leu	Phe	Thr	Val	Ala	Val	Lys	Gly	Gly	Tyr	Glu	Ala	
			340					345					350			
tgc	gtg	aaa	ttg	gtc	aac	aat	ctc	aag	ctg	ttc	agc	cat	gtg	gca	aac	1104
Cys	Val	Lys	Leu	Val	Asn	Asn	Leu	Lys	Leu	Phe	Ser	His	Val	Ala	Asn	
	355						360					365				
ctg	ggc	gac	gcg	cgc	tcg	ctg	atc	atc	cat	tcg	gcc	tcg	acc	acg	cac	1152
Leu	Gly	Asp	Ala	Arg	Ser	Leu	Ile	Ile	His	Ser	Ala	Ser	Thr	Thr	His	
	370					375					380					
cgt	cag	ctg	acc	gag	gaa	cag	cag	atc	aag	gcg	ggg	gcg	gcg	ccg	aat	1200

Arg Gln Leu Thr Glu Glu Gln Gln Ile Lys Ala Gly Ala Ala Pro Asn
 385 390 395 400

gtg gtg cgg ctc tcg atc ggg atc gag aat gcc gcc gat ctg atc gcc 1248
 Val Val Arg Leu Ser Ile Gly Ile Glu Asn Ala Ala Asp Leu Ile Ala
 405 410 415

gat ctg gat cag gct ctg gcc gcc gcc acc gcc tga 1284
 Asp Leu Asp Gln Ala Leu Ala Ala Ala Thr Ala
 420 425

<210> 38
 <211> 427
 <212> PRT
 <213> Rhodobacter capsulatus

<400> 38

Met Thr Asp Gln Ala Phe Asp Thr Leu Gln Ile His Ala Gly Ala Glu
 1 5 10 15

Pro Asp Pro Ala Thr Gly Ala Arg Gln Val Pro Ile Tyr Gln Thr Thr
 20 25 30

Ser Tyr Val Phe Lys Asp Ala Asp His Ala Ala Arg Leu Phe Gly Leu
 35 40 45

Gln Glu Val Gly Tyr Ile Tyr Ser Arg Leu Thr Asn Pro Thr Val Ser
 50 55 60

Ala Leu Ala Ala Arg Val Ala Ala Leu Glu Gly Gly Val Gly Ala Val
 65 70 75 80

Cys Cys Ser Ser Gly His Ala Ala Gln Ile Met Ala Leu Phe Pro Leu
 85 90 95

Met Gly Pro Gly Leu Asn Ile Val Ala Ser Thr Arg Leu Tyr Gly Gly
 100 105 110

Thr Ile Thr Gln Phe Ser Gln Thr Ile Lys Arg Phe Gly Trp Ser Cys
 115 120 125

Thr Phe Val Asp Phe Asp Asp Leu Ala Ala Leu Glu Ala Ala Val Asp
 130 135 140

Asp Asn Thr Arg Ala Ile Phe Cys Glu Ser Ile Ser Asn Pro Gly Gly
 145 150 155 160

Tyr Ile Thr Asp Leu Pro Ala Val Ala Ala Val Ala Asn Lys Val Gly
 165 170 175

Leu Pro Leu Ile Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Cys Arg
 180 185 190
 Pro Ile Glu His Gly Ala Thr Leu Val Val His Ser Ala Thr Lys Tyr
 195 200 205
 Leu Thr Gly Asn Gly Thr Val Thr Gly Gly Val Ile Val Asp Ser Gly
 210 215 220
 Lys Phe Asp Trp Ser Ala Ser Gly Lys Phe Pro Ser Leu Ser Ala Pro
 225 230 235 240
 Glu Pro Ala Tyr His Gly Leu Lys Phe His Glu Ala Leu Gly Pro Met
 245 250 255
 Ala Phe Thr Phe His Ser Ile Ala Val Gly Leu Arg Asp Leu Gly Met
 260 265 270
 Thr Met Asn Pro Gln Gly Ala His Tyr Thr Leu Met Gly Ile Glu Thr
 275 280 285
 Leu Ser Leu Arg Met Asp Lys His Val Ala Asn Ala Lys Ala Val Ala
 290 295 300
 Glu Trp Leu Ala Lys Asp Pro Arg Ile Asp Phe Val Thr Trp Ala Gly
 305 310 315 320
 Leu Pro Ser Ser Pro Trp His Glu Arg Ala Glu Arg Leu Cys Pro Lys
 325 330 335
 Gly Ala Gly Ala Leu Phe Thr Val Ala Val Lys Gly Gly Tyr Glu Ala
 340 345 350
 Cys Val Lys Leu Val Asn Asn Leu Lys Leu Phe Ser His Val Ala Asn
 355 360 365
 Leu Gly Asp Ala Arg Ser Leu Ile Ile His Ser Ala Ser Thr Thr His
 370 375 380
 Arg Gln Leu Thr Glu Glu Gln Gln Ile Lys Ala Gly Ala Ala Pro Asn
 385 390 395 400
 Val Val Arg Leu Ser Ile Gly Ile Glu Asn Ala Ala Asp Leu Ile Ala
 405 410 415
 Asp Leu Asp Gln Ala Leu Ala Ala Ala Thr Ala
 420 425

<210> 39

<211> 1269

<212> DNA

<213> *Pasteurella multocida*

<220>

<221> CDS

<222> (1)..(1269)

<223>

<400> 39

atg gaa ttt gca aca aaa tgt cta cat gcc ggt tat aca ccg aaa aat	48
Met Glu Phe Ala Thr Lys Cys Leu His Ala Gly Tyr Thr Pro Lys Asn	
1 5 10 15	
ggt gag cct cgt gtt caa ccg atc gta caa agt acc act ttt acc tac	96
Gly Glu Pro Arg Val Gln Pro Ile Val Gln Ser Thr Thr Phe Thr Tyr	
20 25 30	
gat tcc gcc gaa gaa att ggt aag tta ttt gat tta caa gcg gct ggc	144
Asp Ser Ala Glu Glu Ile Gly Lys Leu Phe Asp Leu Gln Ala Ala Gly	
35 40 45	
tat ttt tac acc cgc ctt tca aat cct act acc aat gcg gca gaa gaa	192
Tyr Phe Tyr Thr Arg Leu Ser Asn Pro Thr Thr Asn Ala Ala Glu Glu	
50 55 60	
aaa att acc gca ctt gaa ggc ggt gta gca acc atg tgt acc gca tca	240
Lys Ile Thr Ala Leu Glu Gly Gly Val Ala Thr Met Cys Thr Ala Ser	
65 70 75 80	
ggg caa gcc gcc gtg ttt tac gcg atg ctc aat att tta caa gcc ggt	288
Gly Gln Ala Ala Val Phe Tyr Ala Met Leu Asn Ile Leu Gln Ala Gly	
85 90 95	
gat cac ttt att tct tca tcg tat gtt tac ggt ggt agc tac aac tta	336
Asp His Phe Ile Ser Ser Ser Tyr Val Tyr Gly Gly Ser Tyr Asn Leu	
100 105 110	
ttt gca cat acc ttc aaa aaa atg gga att gag gtc act ttt gtg gat	384
Phe Ala His Thr Phe Lys Lys Met Gly Ile Glu Val Thr Phe Val Asp	
115 120 125	
caa gat tta cct ctt gag gaa tta aaa aaa gct att cgc cca aat acg	432
Gln Asp Leu Pro Leu Glu Glu Leu Lys Lys Ala Ile Arg Pro Asn Thr	
130 135 140	
aaa gcc att ttt gcc gaa act att gcc aat ccc gca tta cgc gtg ttg	480
Lys Ala Ile Phe Ala Glu Thr Ile Ala Asn Pro Ala Leu Arg Val Leu	
145 150 155 160	
gat att gaa aag ttt gtt gca ctt gcg aag gca gca caa gcc cct tta	528
Asp Ile Glu Lys Phe Val Ala Leu Ala Lys Ala Ala Gln Ala Pro Leu	
165 170 175	
tta gtt gac aat act ttt gca acc ccg tat ttt tgt cgc cct atc gaa	576
Leu Val Asp Asn Thr Phe Ala Thr Pro Tyr Phe Cys Arg Pro Ile Glu	
180 185 190	

ttt ggt gct aac gtg gta att cat agt acg tca aaa tat tta gat ggg Phe Gly Ala Asn Val Val Ile His Ser Thr Ser Lys Tyr Leu Asp Gly 195 200 205	624
cat gcg att gcg ttg gga ggt tcg atc aca gat ggc ggg aat ttt gat His Ala Ile Ala Leu Gly Gly Ser Ile Thr Asp Gly Gly Asn Phe Asp 210 215 220	672
tgg aat aat ggt aaa ttc cca caa tta agc aca cct gat caa act tat Trp Asn Asn Gly Lys Phe Pro Gln Leu Ser Thr Pro Asp Gln Thr Tyr 225 230 235 240	720
cac ggt tta gtt tat acc gaa acc ttt gtt cca gcc gct tat att gtc His Gly Leu Val Tyr Thr Glu Thr Phe Val Pro Ala Ala Tyr Ile Val 245 250 255	768
aaa gcc cgt gtg caa tta atg cgt gat tta ggt gcc aca cca gca cca Lys Ala Arg Val Gln Leu Met Arg Asp Leu Gly Ala Thr Pro Ala Pro 260 265 270	816
caa aat agt ttc ttg ctc aat gtg ggc atg gaa act ctt gca ctg cgt Gln Asn Ser Phe Leu Leu Asn Val Gly Met Glu Thr Leu Ala Leu Arg 275 280 285	864
atg caa cgt cat tat gaa aat gca caa gcg gtc gcc gaa ttt tta gaa Met Gln Arg His Tyr Glu Asn Ala Gln Ala Val Ala Glu Phe Leu Glu 290 295 300	912
aat cat cca caa gtg gca aaa gtg agt tat ccg ggc ttg gca agt tca Asn His Pro Gln Val Ala Lys Val Ser Tyr Pro Gly Leu Ala Ser Ser 305 310 315 320	960
cct gat cat gca cta aaa caa aaa tat tta cca aac ggt tta tgt ggt Pro Asp His Ala Leu Lys Gln Lys Tyr Leu Pro Asn Gly Leu Cys Gly 325 330 335	1008
gtg att tcc ttt gaa att aga ggg gga aga gaa act gca gca aaa tgg Val Ile Ser Phe Glu Ile Arg Gly Gly Arg Glu Thr Ala Ala Lys Trp 340 345 350	1056
ctg aat gcg cta caa ctg gct tct cgt gaa gtc cat gta gcg gat att Leu Asn Ala Leu Gln Leu Ala Ser Arg Glu Val His Val Ala Asp Ile 355 360 365	1104
cgc act tgt gct tta cat ccg gcg acg tca aca cac cgt caa tta agt Arg Thr Cys Ala Leu His Pro Ala Thr Ser Thr His Arg Gln Leu Ser 370 375 380	1152
gag gct gaa tta gaa aaa gtg ggg att tct gcg ggt tta att cgt ctt Glu Ala Glu Leu Glu Lys Val Gly Ile Ser Ala Gly Leu Ile Arg Leu 385 390 395 400	1200
tct tgc ggt att gaa agt atc caa gat att ttg gct gac tta gaa caa Ser Cys Gly Ile Glu Ser Ile Gln Asp Ile Leu Ala Asp Leu Glu Gln 405 410 415	1248
gca ttc cac gcg gca aaa taa Ala Phe His Ala Ala Lys 420	1269

<210> 40

<211> 422

<212> PRT

<213> *Pasteurella multocida*

<400> 40

Met Glu Phe Ala Thr Lys Cys Leu His Ala Gly Tyr Thr Pro Lys Asn
 1 5 10 15
 Gly Glu Pro Arg Val Gln Pro Ile Val Gln Ser Thr Thr Phe Thr Tyr
 20 25 30
 Asp Ser Ala Glu Glu Ile Gly Lys Leu Phe Asp Leu Gln Ala Ala Gly
 35 40 45
 Tyr Phe Tyr Thr Arg Leu Ser Asn Pro Thr Thr Asn Ala Ala Glu Glu
 50 55 60
 Lys Ile Thr Ala Leu Glu Gly Gly Val Ala Thr Met Cys Thr Ala Ser
 65 70 75 80
 Gly Gln Ala Ala Val Phe Tyr Ala Met Leu Asn Ile Leu Gln Ala Gly
 85 90 95
 Asp His Phe Ile Ser Ser Ser Tyr Val Tyr Gly Gly Ser Tyr Asn Leu
 100 105 110
 Phe Ala His Thr Phe Lys Lys Met Gly Ile Glu Val Thr Phe Val Asp
 115 120 125
 Gln Asp Leu Pro Leu Glu Glu Leu Lys Lys Ala Ile Arg Pro Asn Thr
 130 135 140
 Lys Ala Ile Phe Ala Glu Thr Ile Ala Asn Pro Ala Leu Arg Val Leu
 145 150 155 160
 Asp Ile Glu Lys Phe Val Ala Leu Ala Lys Ala Ala Gln Ala Pro Leu
 165 170 175
 Leu Val Asp Asn Thr Phe Ala Thr Pro Tyr Phe Cys Arg Pro Ile Glu
 180 185 190
 Phe Gly Ala Asn Val Val Ile His Ser Thr Ser Lys Tyr Leu Asp Gly
 195 200 205
 His Ala Ile Ala Leu Gly Gly Ser Ile Thr Asp Gly Gly Asn Phe Asp
 210 215 220
 Trp Asn Asn Gly Lys Phe Pro Gln Leu Ser Thr Pro Asp Gln Thr Tyr
 225 230 235 240
 His Gly Leu Val Tyr Thr Glu Thr Phe Val Pro Ala Ala Tyr Ile Val

	245		250		255										
Lys	Ala	Arg	Val	Gln	Leu	Met	Arg	Asp	Leu	Gly	Ala	Thr	Pro	Ala	Pro
	260							265					270		
Gln	Asn	Ser	Phe	Leu	Leu	Asn	Val	Gly	Met	Glu	Thr	Leu	Ala	Leu	Arg
	275						280						285		
Met	Gln	Arg	His	Tyr	Glu	Asn	Ala	Gln	Ala	Val	Ala	Glu	Phe	Leu	Glu
	290					295						300			
Asn	His	Pro	Gln	Val	Ala	Lys	Val	Ser	Tyr	Pro	Gly	Leu	Ala	Ser	Ser
305					310					315					320
Pro	Asp	His	Ala	Leu	Lys	Gln	Lys	Tyr	Leu	Pro	Asn	Gly	Leu	Cys	Gly
				325					330					335	
Val	Ile	Ser	Phe	Glu	Ile	Arg	Gly	Gly	Arg	Glu	Thr	Ala	Ala	Lys	Trp
			340					345						350	
Leu	Asn	Ala	Leu	Gln	Leu	Ala	Ser	Arg	Glu	Val	His	Val	Ala	Asp	Ile
	355						360					365			
Arg	Thr	Cys	Ala	Leu	His	Pro	Ala	Thr	Ser	Thr	His	Arg	Gln	Leu	Ser
	370					375						380			
Glu	Ala	Glu	Leu	Glu	Lys	Val	Gly	Ile	Ser	Ala	Gly	Leu	Ile	Arg	Leu
385					390					395					400
Ser	Cys	Gly	Ile	Glu	Ser	Ile	Gln	Asp	Ile	Leu	Ala	Asp	Leu	Glu	Gln
				405					410					415	
Ala	Phe	His	Ala	Ala	Lys										
			420												

<210> 41

<211> 1266

<212> DNA

<213> Clostridium difficile

<220>

<221> CDS

<222> (1)..(1266)

<223>

<400>	41															
atg Met 1	tat Tyr	aat Asn	aaa Lys	gaa Glu 5	aca Thr	ata Ile	tgt Cys	gtg Val	caa Gln 10	gga Gly	aat Asn	tat Tyr	aaa Lys	cca Pro 15	ggt Gly	48
aat Asn	gga Gly	gaa Glu 20	cca Pro	aga Arg	gta Val	cta Leu	cct Pro	tta Leu 25	tat Tyr	caa Gln	agt Ser	aca Thr	act Thr 30	ttt Phe	aaa Lys	96
tat Tyr	agc Ser	agt Ser 35	ata Ile	gac Asp	caa Gln	ctt Leu	gct Ala 40	gaa Glu	tta Leu	ttt Phe	gat Asp 45	tta Leu	aaa Lys	gtt Val	gat Asp	144
gga Gly	cat His 50	ata Ile	tat Tyr	tca Ser	aga Arg	ata Ile 55	agc Ser	aat Asn	cct Pro	act Thr	att Ile 60	caa Gln	gct Ala	ttt Phe	gaa Glu	192
gaa Glu 65	aaa Lys	ata Ile	agt Ser	tta Leu	cta Leu 70	gag Glu	ggg Gly	gga Gly	gta Val	tct Ser 75	tct Ser	gta Val	gct Ala	gta Val 80	tca Ser	240
tca Ser	ggg Gly	caa Gln	tct Ser	gca Ala 85	aat Asn	atg Met	ttg Leu	gca Ala	gtt Val 90	tta Leu	aat Asn	ata Ile	tgt Cys	aaa Lys 95	tca Ser	288
gga Gly	gat Asp	agt Ser 100	ata Ile	ctt Leu	tgt Cys	tct Ser	tca Ser	aaa Lys 105	gta Val	tat Tyr	gga Gly	gga Gly	aca Thr 110	ttc Phe	aat Asn	336
tta Leu	cta Leu	gga Gly 115	cct Pro	agt Ser	ctt Leu	aaa Lys	aaa Lys 120	ttt Phe	ggg Gly	ata Ile	gat Asp	tta Leu 125	ata Ile	tcg Ser	ttt Phe	384
gac Asp	tta Leu 130	gat Asp	tca Ser	agt Ser	gaa Glu	gat Asp 135	gag Glu	ata Ile	gta Val	gaa Glu	ctt Leu 140	gca Ala	aag Lys	gaa Glu	aat Asn	432
act Thr 145	aag Lys	gtt Val	gtg Val	ttt Phe	gca Ala 150	gaa Glu	aca Thr	ctt Leu	gca Ala	aat Asn 155	cca Pro	act Thr	ctt Leu	gaa Glu	gtc Val 160	480
ata Ile	gat Asp	ttt Phe	gaa Glu	aaa Lys 165	ata Ile	gca Ala	aat Asn	gta Val	gct Ala 170	aag Lys	aga Arg	att Ile	aat Asn	gtt Val 175	cca Pro	528
ttt Phe	att Ile	gtt Val	gat Asp 180	aat Asn	tca Ser	tta Leu	gca Ala	tct Ser 185	cca Pro	gtg Val	ctt Leu	tgt Cys	aac Asn 190	cct Pro	tta Leu	576
aag Lys	tat Tyr	gga Gly 195	gca Ala	aat Asn	ata Ile	gtt Val	act Thr 200	cat His	tct Ser	acc Thr	aca Thr	aaa Lys 205	tat Tyr	tta Leu	gat Asp	624
ggg Gly	cat His 210	gct Ala	tca Ser	agt Ser	gtt Val	gga Gly 215	gga Gly	att Ile	ata Ile	gtg Val	gat Asp 220	ggg Gly	gga Gly	aac Asn	ttt Phe	672
aac Asn 225	tgg Trp	gat Asp	aat Asn	gga Gly	aaa Lys 230	ttt Phe	cca Pro	gaa Glu	tta Leu	gtt Val 235	gag Glu	cca Pro	gac Asp	cca Pro	aca Thr 240	720
tat Tyr	cat His	ggg Gly	ata Ile	agc Ser 245	tat Tyr	act Thr	caa Gln	aaa Lys	ttt Phe 250	gga Gly	aat Asn	gcc Ala	gca Ala	tat Tyr 255	gca Ala	768
act Thr	aaa Lys	gca Ala	aga Arg	gtt Val	cag Gln	ttg Leu	ctt Leu	aga Arg	gac Asp	tat Tyr	gga Gly	aat Asn	tgt Cys	tta Leu	agc Ser	816

260	265	270	
cca ttc aat gcg tat ctt act aat tta aat gtt gaa aca cta cat ctt Pro Phe Asn Ala Tyr Leu Thr Asn Leu Asn Val Glu Thr Leu His Leu 275 280 285			864
aga atg gag aga cat agt gaa aat gca ctt aaa ata gct aga ttt tta Arg Met Glu Arg His Ser Glu Asn Ala Leu Lys Ile Ala Arg Phe Leu 290 295 300			912
gaa aaa cat gaa aat gta gat tgg att aat tac cca gga ctt gaa gat Glu Lys His Glu Asn Val Asp Trp Ile Asn Tyr Pro Gly Leu Glu Asp 305 310 315 320			960
aac aag tat tat gag aat gcc aaa aag tat tta tca aga gga tgt agt Asn Lys Tyr Tyr Glu Asn Ala Lys Lys Tyr Leu Ser Arg Gly Cys Ser 325 330 335			1008
ggg gtt tta tca ttt gga gta aga ggt ggg tta gaa aat gcc aaa aaa Gly Val Leu Ser Phe Gly Val Arg Gly Gly Leu Glu Asn Ala Lys Lys 340 345 350			1056
ttt gtg gaa aaa tta cag ata gca tct ttg gtt aca cat gtt tca gat Phe Val Glu Lys Leu Gln Ile Ala Ser Leu Val Thr His Val Ser Asp 355 360 365			1104
gta aga act tgt gtt ata cat cca gct tca act act cat aga caa tta Val Arg Thr Cys Val Ile His Pro Ala Ser Thr Thr His Arg Gln Leu 370 375 380			1152
aca gaa gaa caa tta att gca tct gga gta ttg cct tca cta ata aga Thr Glu Glu Gln Leu Ile Ala Ser Gly Val Leu Pro Ser Leu Ile Arg 385 390 395 400			1200
tta tct gtt gga ata gaa aat gta gag gat tta ata gct gat tta aat Leu Ser Val Gly Ile Glu Asn Val Glu Asp Leu Ile Ala Asp Leu Asn 405 410 415			1248
caa gct tta aat ttc taa Gln Ala Leu Asn Phe 420			1266

<210> 42

<211> 421

<212> PRT

<213> Clostridium difficile

<400> 42

Met Tyr Asn Lys Glu Thr Ile Cys Val Gln Gly Asn Tyr Lys Pro Gly 1 5 10 15
Asn Gly Glu Pro Arg Val Leu Pro Leu Tyr Gln Ser Thr Thr Phe Lys 20 25 30
Tyr Ser Ser Ile Asp Gln Leu Ala Glu Leu Phe Asp Leu Lys Val Asp 35 40 45

Gly His Ile Tyr Ser Arg Ile Ser Asn Pro Thr Ile Gln Ala Phe Glu
 50 55 60
 Glu Lys Ile Ser Leu Leu Glu Gly Gly Val Ser Ser Val Ala Val Ser
 65 70 75 80
 Ser Gly Gln Ser Ala Asn Met Leu Ala Val Leu Asn Ile Cys Lys Ser
 85 90 95
 Gly Asp Ser Ile Leu Cys Ser Ser Lys Val Tyr Gly Gly Thr Phe Asn
 100 105 110
 Leu Leu Gly Pro Ser Leu Lys Lys Phe Gly Ile Asp Leu Ile Ser Phe
 115 120 125
 Asp Leu Asp Ser Ser Glu Asp Glu Ile Val Glu Leu Ala Lys Glu Asn
 130 135 140
 Thr Lys Val Val Phe Ala Glu Thr Leu Ala Asn Pro Thr Leu Glu Val
 145 150 155 160
 Ile Asp Phe Glu Lys Ile Ala Asn Val Ala Lys Arg Ile Asn Val Pro
 165 170 175
 Phe Ile Val Asp Asn Ser Leu Ala Ser Pro Val Leu Cys Asn Pro Leu
 180 185 190
 Lys Tyr Gly Ala Asn Ile Val Thr His Ser Thr Thr Lys Tyr Leu Asp
 195 200 205
 Gly His Ala Ser Ser Val Gly Gly Ile Ile Val Asp Gly Gly Asn Phe
 210 215 220
 Asn Trp Asp Asn Gly Lys Phe Pro Glu Leu Val Glu Pro Asp Pro Thr
 225 230 235 240
 Tyr His Gly Ile Ser Tyr Thr Gln Lys Phe Gly Asn Ala Ala Tyr Ala
 245 250 255
 Thr Lys Ala Arg Val Gln Leu Leu Arg Asp Tyr Gly Asn Cys Leu Ser
 260 265 270
 Pro Phe Asn Ala Tyr Leu Thr Asn Leu Asn Val Glu Thr Leu His Leu
 275 280 285
 Arg Met Glu Arg His Ser Glu Asn Ala Leu Lys Ile Ala Arg Phe Leu
 290 295 300
 Glu Lys His Glu Asn Val Asp Trp Ile Asn Tyr Pro Gly Leu Glu Asp
 305 310 315 320

Asn Lys Tyr Tyr Glu Asn Ala Lys Lys Tyr Leu Ser Arg Gly Cys Ser
 325 330 335

Gly Val Leu Ser Phe Gly Val Arg Gly Gly Leu Glu Asn Ala Lys Lys
 340 345 350

Phe Val Glu Lys Leu Gln Ile Ala Ser Leu Val Thr His Val Ser Asp
 355 360 365

Val Arg Thr Cys Val Ile His Pro Ala Ser Thr Thr His Arg Gln Leu
 370 375 380

Thr Glu Glu Gln Leu Ile Ala Ser Gly Val Leu Pro Ser Leu Ile Arg
 385 390 395 400

Leu Ser Val Gly Ile Glu Asn Val Glu Asp Leu Ile Ala Asp Leu Asn
 405 410 415

Gln Ala Leu Asn Phe
 420

<210> 43

<211> 1272

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1272)

<223>

<400> 43
 atg aat ttc aat aaa gaa act tta gca tta cac gga gct tat aat ttt 48
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 1 5 10 15
 gat act caa aga agt att agt gtg cct ata tat caa aac act gcg tat 96
 Asp Thr Gln Arg Ser Ile Ser Val Pro Ile Tyr Gln Asn Thr Ala Tyr
 20 25 30
 aat ttt gaa aat ttg gat caa gct gca gca agg ttt aat ctt caa gaa 144
 Asn Phe Glu Asn Leu Asp Gln Ala Ala Ala Arg Phe Asn Leu Gln Glu
 35 40 45
 ctt ggc aat att tac tca aga ctt agc aat cct aca agc gat gtt tta 192
 Leu Gly Asn Ile Tyr Ser Arg Leu Ser Asn Pro Thr Ser Asp Val Leu
 50 55 60
 gga caa aga ctt gct aat gtc gaa gga ggg gct ttt gga att cct gtt 240

Gly 65	Gln	Arg	Leu	Ala	Asn 70	Val	Glu	Gly	Gly	Ala 75	Phe	Gly	Ile	Pro	Val 80	
gct Ala	agc Ser	ggg Gly	atg Met	gca Ala	gct Ala	tgt Cys	ttt Phe	tat Tyr	gct Ala	ctt Leu	atc Ile	aat Asn	tta Leu	gca Ala	agt Ser	288
tcg Ser	gga Gly	gat Asp	aat Asn	gtc Val	gcg Ala	tat Tyr	tcg Ser	aac Asn	aaa Lys	att Ile	tat Tyr	ggg Gly	ggg Gly	act Thr	caa Gln	336
act Thr	tta Leu	att Ile	tct Ser	cac His	aca Thr	ctt Leu	aaa Lys	aat Asn	ttt Phe	ggc Gly	ata Ile	gaa Glu	gct Ala	agg Arg	gaa Glu	384
ttt Phe	gat Asp	atc Ile	gat Asp	gat Asp	tta Leu	gat Asp	agc Ser	ttg Leu	gaa Glu	aaa Lys	ggt Val	ata Ile	gat Asp	caa Gln	aac Asn	432
aca Thr	aaa Lys	gcg Ala	att Ile	ttt Phe	ttc Phe	gaa Glu	agt Ser	ctt Leu	tca Ser	aat Asn	cct Pro	caa Gln	att Ile	gcc Ala	ata Ile	480
gct Ala	gat Asp	ata Ile	gaa Glu	aaa Lys	ata Ile	aac Asn	caa Gln	ata Ile	gca Ala	aaa Lys	aaa Lys	cat His	aaa Lys	atc Ile	gtt Val	528
agc Ser	att Ile	tgt Cys	gat Asp	aat Asn	acc Thr	gtt Val	gct Ala	act Thr	cct Pro	ttc Phe	tta Leu	ctc Leu	caa Gln	cct Pro	ttt Phe	576
aaa Lys	cat His	ggc Gly	gtg Val	gat Asp	gta Val	atc Ile	gtg Val	cat His	agt Ser	tta Leu	agt Ser	aaa Lys	tat Tyr	gta Val	agc Ser	624
ggg Gly	caa Gln	ggc Gly	act Thr	gct Ala	ttg Leu	ggg Gly	gga Gly	gca Ala	ctt Leu	ata Ile	gaa Glu	aga Arg	aaa Lys	gat Asp	tta Leu	672
aac Asn	gac Asp	ttg Leu	ctt Leu	aaa Lys	aat Asn	aac Asn	gat Asp	aga Arg	tat Tyr	aaa Lys	gct Ala	ttt Phe	aac Asn	act Thr	cct Pro	720
gat Asp	cca Pro	agt Ser	tat Tyr	cat His	gga Gly	ctg Leu	aat Asn	tta Leu	aat Asn	aca Thr	ctt Leu	gat Asp	ttg Leu	ccg Pro	att Ile	768
ttt Phe	agt Ser	att Ile	aga Arg	gtc Val	atc Ile	atc Ile	act Thr	tgg Trp	ctt Leu	aga Arg	gat Asp	cta Leu	gga Gly	gct Ala	agc Ser	816
tta Leu	gca Ala	cct Pro	caa Gln	aat Asn	gct Ala	tgg Trp	tta Leu	ctt Leu	tta Leu	caa Gln	gga Gly	ctt Leu	gaa Glu	acc Thr	ttg Leu	864
gca Ala	gtg Val	cgt Arg	ata Ile	gaa Glu	aaa Lys	cac His	agt Ser	caa Gln	aat Asn	gct Ala	gaa Glu	aaa Lys	gtt Val	gcg Ala	aat Asn	912
ttt Phe	tta Leu	aat Asn	tct Ser	cat His	cct Pro	gat Asp	atc Ile	aag Lys	ggc Gly	gta Val	aat Asn	tat Tyr	cct Pro	act Thr	tta Leu	960
gca Ala	agt Ser	aat Asn	gct Ala	tat Tyr	cat His	aat Asn	tta Leu	ttt Phe	aaa Lys	aaa Lys	tat Tyr	ttt Phe	gat Asp	aaa Lys	aat Asn	1008

ttt gct agc ggg ctt tta agc ttt gaa gct aaa gat tat gag cat gct 1056
 Phe Ala Ser Gly Leu Leu Ser Phe Glu Ala Lys Asp Tyr Glu His Ala
 340 345 350
 aga aga att tgt gat aaa act caa ctt ttc tta ctt gct gca aat ttg 1104
 Arg Arg Ile Cys Asp Lys Thr Gln Leu Phe Leu Leu Ala Ala Asn Leu
 355 360 365
 ggt gat agc aag tct ttg atc atc cat cct gct tct act act cat tcg 1152
 Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser Thr Thr His Ser
 370 375 380
 caa cta agc gaa gaa gaa ctc caa aaa gca ggc att acg aaa gct act 1200
 Gln Leu Ser Glu Glu Glu Leu Gln Lys Ala Gly Ile Thr Lys Ala Thr
 385 390 395 400
 ata cgc tta agc ata gga ctt gaa aat agc gat gat ttg ata gcg gat 1248
 Ile Arg Leu Ser Ile Gly Leu Glu Asn Ser Asp Asp Leu Ile Ala Asp
 405 410 415
 tta aaa caa gct ata gaa agt taa 1272
 Leu Lys Gln Ala Ile Glu Ser
 420

<210> 44

<211> 423

<212> PRT

<213> Campylobacter jejuni

<400> 44

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 Asn Phe Glu Asn Leu Asp Gln Ala Ala Ala Arg Phe Asn Leu Gln Glu
 35 40 45
 Leu Gly Asn Ile Tyr Ser Arg Leu Ser Asn Pro Thr Ser Asp Val Leu
 50 55 60
 Gly Gln Arg Leu Ala Asn Val Glu Gly Gly Ala Phe Gly Ile Pro Val
 65 70 75 80
 Ala Ser Gly Met Ala Ala Cys Phe Tyr Ala Leu Ile Asn Leu Ala Ser
 85 90 95
 Ser Gly Asp Asn Val Ala Tyr Ser Asn Lys Ile Tyr Gly Gly Thr Gln
 100 105 110
 Thr Leu Ile Ser His Thr Leu Lys Asn Phe Gly Ile Glu Ala Arg Glu
 115 120 125

Phe Asp Ile Asp Asp Leu Asp Ser Leu Glu Lys Val Ile Asp Gln Asn
 130 135 140
 Thr Lys Ala Ile Phe Phe Glu Ser Leu Ser Asn Pro Gln Ile Ala Ile
 145 150 155 160
 Ala Asp Ile Glu Lys Ile Asn Gln Ile Ala Lys Lys His Lys Ile Val
 165 170 175
 Ser Ile Cys Asp Asn Thr Val Ala Thr Pro Phe Leu Leu Gln Pro Phe
 180 185 190
 Lys His Gly Val Asp Val Ile Val His Ser Leu Ser Lys Tyr Val Ser
 195 200 205
 Gly Gln Gly Thr Ala Leu Gly Gly Ala Leu Ile Glu Arg Lys Asp Leu
 210 215 220
 Asn Asp Leu Leu Lys Asn Asn Asp Arg Tyr Lys Ala Phe Asn Thr Pro
 225 230 235 240
 Asp Pro Ser Tyr His Gly Leu Asn Leu Asn Thr Leu Asp Leu Pro Ile
 245 250 255
 Phe Ser Ile Arg Val Ile Ile Thr Trp Leu Arg Asp Leu Gly Ala Ser
 260 265 270
 Leu Ala Pro Gln Asn Ala Trp Leu Leu Leu Gln Gly Leu Glu Thr Leu
 275 280 285
 Ala Val Arg Ile Glu Lys His Ser Gln Asn Ala Glu Lys Val Ala Asn
 290 295 300
 Phe Leu Asn Ser His Pro Asp Ile Lys Gly Val Asn Tyr Pro Thr Leu
 305 310 315 320
 Ala Ser Asn Ala Tyr His Asn Leu Phe Lys Lys Tyr Phe Asp Lys Asn
 325 330 335
 Phe Ala Ser Gly Leu Leu Ser Phe Glu Ala Lys Asp Tyr Glu His Ala
 340 345 350
 Arg Arg Ile Cys Asp Lys Thr Gln Leu Phe Leu Leu Ala Ala Asn Leu
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 Gly Asp Ser Lys Ser Leu Ile Ile His Pro Ala Ser Thr Thr His Ser
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 Gln Leu Ser Glu Glu Glu Leu Gln Lys Ala Gly Ile Thr Lys Ala Thr

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<212>	DNA
<213>	Streptococcus pneumoniae

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<222>   (1) .. (1041)  
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Leu Arg Lys Pro Gly Asn Ile Tyr Thr Arg Ile Thr Asn Pro Thr Thr																		
1	5																10	15
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gct gcc ctt gaa ggt ggt gtt gaa gcg cta gca aca gca tca ggt atg																	96	
Ala Ala Leu Glu Gly Gly Val Glu Ala Leu Ala Thr Ala Ser Gly Met																		
	20																25	30
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act gca gtg act tat acg att ttg gcg att gcc cat gct ggt gac cat																	144	
Thr Ala Val Thr Tyr Thr Ile Leu Ala Ile Ala His Ala Gly Asp His																		
	35																40	45
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gta gtg gct gct tcg act att tac ggt gga acc ttc aat ctt ttg aaa																	192	
Val Val Ala Ala Ser Thr Ile Tyr Gly Gly Thr Phe Asn Leu Leu Lys																		
	50																55	60
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gaa ccc ctt cct cgt tat ggt atc aca aca acc ttt ttc gat att gat																	240	
Glu Pro Leu Pro Arg Tyr Gly Ile Thr Thr Thr Phe Phe Asp Ile Asp																		
65	70																75	80
<hr/>																		
aat ttg gag gaa gta gaa gca gct atc aaa gac aat acc aag ctt gtc																	288	
Asn Leu Glu Glu Val Glu Ala Ala Ile Lys Asp Asn Thr Lys Leu Val																		
	85																90	95
<hr/>																		
ttg att gaa acc ttg ggt aac ccc ttg att aat att cca gac ctg gaa																	336	
Leu Ile Glu Thr Leu Gly Asn Pro Leu Ile Asn Ile Pro Asp Leu Glu																		
	100																105	110
<hr/>																		
aaa ctg gca gag att gct cat aaa cat caa atc cca ctt gtg tca gac																	384	
Lys Leu Ala Glu Ile Ala His Lys His Gln Ile Pro Leu Val Ser Asp																		
	115																120	125
<hr/>																		
aat act ttt gca aca cct tat ttg att aac gtc ttc tct cat ggc gtt																	432	
Asn Thr Phe Ala Thr Pro Tyr Leu Ile Asn Val Phe Ser His Gly Val																		
	130																135	140

gac att gcc att cac tct gtg act aag ttt atc ggt ggg cat ggt aca Asp Ile Ala Ile His Ser Val Thr Lys Phe Ile Gly Gly His Gly Thr 145 150 155 160	480
act att gga gga ata att gtc gat agt ggt cgt ttt gac tgg acg gct Thr Ile Gly Gly Ile Ile Val Asp Ser Gly Arg Phe Asp Trp Thr Ala 165 170 175	528
tca ggg aaa ttc cct caa ttt gtt gac gag ggt cca agc tgc cac aat Ser Gly Lys Phe Pro Gln Phe Val Asp Glu Gly Pro Ser Cys His Asn 180 185 190	576
ttg agc tat act cgt gat gtg ggt gca gca gcc ttt att ata gct gtt Leu Ser Tyr Thr Arg Asp Val Gly Ala Ala Ala Phe Ile Ile Ala Val 195 200 205	624
cga gtt caa ttg ctt cgt gat aca ggt gca gcc ttg tca cca ttc aat Arg Val Gln Leu Leu Arg Asp Thr Gly Ala Ala Leu Ser Pro Phe Asn 210 215 220	672
gct ttc ctc ttg cta caa aga ctt gaa acc tct tca ctt cgt gtg gaa Ala Phe Leu Leu Leu Gln Arg Leu Glu Thr Ser Ser Leu Arg Val Glu 225 230 235 240	720
cgc cat gta caa aat gct gag aca att gtt gat ttt ctt gtc aac cat Arg His Val Gln Asn Ala Glu Thr Ile Val Asp Phe Leu Val Asn His 245 250 255	768
cct aag gta gaa aag gta aat tat cca aaa ctt gca gat agt cct tat Pro Lys Val Glu Lys Val Asn Tyr Pro Lys Leu Ala Asp Ser Pro Tyr 260 265 270	816
cat gcc ttg gct gag aaa tac ttg cca aaa ggt gtc ggt tca atc ttt His Ala Leu Ala Glu Lys Tyr Leu Pro Lys Gly Val Gly Ser Ile Phe 275 280 285	864
acc ttc cac gtc aaa ggt ggc gag gaa gaa gca cgc aag gtc att gat Thr Phe His Val Lys Gly Gly Glu Glu Glu Ala Arg Lys Val Ile Asp 290 295 300	912
aat tta gaa atc ttt tct gac ctt gca aac gcg gca gat gct aaa tcg Asn Leu Glu Ile Phe Ser Asp Leu Ala Asn Ala Ala Asp Ala Lys Ser 305 310 315 320	960
ctt gtt gtc cat cca gca aca acc act cac ggt caa ttg tca gaa aaa Leu Val Val His Pro Ala Thr Thr Thr His Gly Gln Leu Ser Glu Lys 325 330 335	1008
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<210> 46

<211> 346

<212> PRT

<213> Streptococcus pneumoniae

<400> 46

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			20					25					30					
Thr	Ala	Val	Thr	Tyr	Thr	Ile	Leu	Ala	Ile	Ala	His	Ala	Gly	Asp	His			
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Val	Val	Ala	Ala	Ser	Thr	Ile	Tyr	Gly	Gly	Thr	Phe	Asn	Leu	Leu	Lys			
	50					55					60							
Glu	Pro	Leu	Pro	Arg	Tyr	Gly	Ile	Thr	Thr	Thr	Phe	Phe	Asp	Ile	Asp			
65					70					75					80			
Asn	Leu	Glu	Glu	Val	Glu	Ala	Ala	Ile	Lys	Asp	Asn	Thr	Lys	Leu	Val			
				85					90					95				
Leu	Ile	Glu	Thr	Leu	Gly	Asn	Pro	Leu	Ile	Asn	Ile	Pro	Asp	Leu	Glu			
			100					105					110					
Lys	Leu	Ala	Glu	Ile	Ala	His	Lys	His	Gln	Ile	Pro	Leu	Val	Ser	Asp			
		115					120					125						
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Asp	Ile	Ala	Ile	His	Ser	Val	Thr	Lys	Phe	Ile	Gly	Gly	His	Gly	Thr			
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Thr	Ile	Gly	Gly	Ile	Ile	Val	Asp	Ser	Gly	Arg	Phe	Asp	Trp	Thr	Ala			
				165					170					175				
Ser	Gly	Lys	Phe	Pro	Gln	Phe	Val	Asp	Glu	Gly	Pro	Ser	Cys	His	Asn			
			180					185					190					
Leu	Ser	Tyr	Thr	Arg	Asp	Val	Gly	Ala	Ala	Ala	Phe	Ile	Ile	Ala	Val			
		195					200					205						
Arg	Val	Gln	Leu	Leu	Arg	Asp	Thr	Gly	Ala	Ala	Leu	Ser	Pro	Phe	Asn			
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Ala	Phe	Leu	Leu	Leu	Gln	Arg	Leu	Glu	Thr	Ser	Ser	Leu	Arg	Val	Glu			
225					230					235					240			
Arg	His	Val	Gln	Asn	Ala	Glu	Thr	Ile	Val	Asp	Phe	Leu	Val	Asn	His			
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Pro	Lys	Val	Glu	Lys	Val	Asn	Tyr	Pro	Lys	Leu	Ala	Asp	Ser	Pro	Tyr			
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His Ala Leu Ala Glu Lys Tyr Leu Pro Lys Gly Val Gly Ser Ile Phe
 275 280 285

Thr Phe His Val Lys Gly Gly Glu Glu Glu Ala Arg Lys Val Ile Asp
 290 295 300

Asn Leu Glu Ile Phe Ser Asp Leu Ala Asn Ala Ala Asp Ala Lys Ser
 305 310 315 320

Leu Val Val His Pro Ala Thr Thr Thr His Gly Gln Leu Ser Glu Lys
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Asp Leu Glu Ala Ala Gly Val Thr Pro Asn
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<210> 47

<211> 1335

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1335)

<223>

<400> 47

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Pro Gly Asp Asn Ala His Arg Ser Arg Ala Val Pro Ile Tyr Ala Thr	
20 25 30	

act tct tat gtt ttc gaa aac tct aag cat ggt tcg caa ttg ttt ggt	144
Thr Ser Tyr Val Phe Glu Asn Ser Lys His Gly Ser Gln Leu Phe Gly	
35 40 45	

cta gaa gtt cca ggt tac gtc tat tcc cgt ttc caa aac cca acc agt	192
Leu Glu Val Pro Gly Tyr Val Tyr Ser Arg Phe Gln Asn Pro Thr Ser	
50 55 60	

aat gtt ttg gaa gaa aga att gct gct tta gaa ggt ggt gct gct gct	240
Asn Val Leu Glu Glu Arg Ile Ala Ala Leu Glu Gly Gly Ala Ala Ala	
65 70 75 80	

ttg gct gtt tcc tcc ggt caa gcc gct caa acc ctt gcc atc caa ggt	288
Leu Ala Val Ser Ser Gly Gln Ala Ala Gln Thr Leu Ala Ile Gln Gly	
85 90 95	

ttg gca cac act ggt gac aac atc gtt tcc act tct tac tta tac ggt	336
Leu Ala His Thr Gly Asp Asn Ile Val Ser Thr Ser Tyr Leu Tyr Gly	

			100				105				110							
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gct Ala	aga Arg 130	ttt Phe	gtt Val	gaa Glu	ggg Gly	gac Asp 135	aat Asn	cca Pro	gaa Glu	gaa Glu	ttc Phe 140	gaa Glu	aag Lys	gtc Val	ttt Phe	432		
gat Asp 145	gaa Glu	aga Arg	acc Thr	aag Lys	gct Ala 150	gtt Val	tat Tyr	ttg Leu	gaa Glu	acc Thr 155	att Ile	ggg Gly	aat Asn	cca Pro	aag Lys 160	480		
tac Tyr	aat Asn	gtt Val	ccg Pro	gat Asp 165	ttt Phe	gaa Glu	aaa Lys	att Ile 170	gtt Val	gca Ala	att Ile	gct Ala	cac His	aaa Lys 175	cac His	528		
ggt Gly	att Ile	cca Pro	gtt Val 180	gtc Val	gtt Val	gac Asp	aac Asn	aca Thr 185	ttt Phe	ggg Gly	gcc Ala	ggg Gly 190	ggg Gly	tac Tyr	ttc Phe	576		
tgt Cys	cag Gln	cca Pro 195	att Ile	aaa Lys	tac Tyr	ggg Gly	gct Ala 200	gat Asp	att Ile	gta Val	aca Thr 205	cat His 210	tct Ser	gct Ala	acc Thr	624		
aaa Lys	tgg Trp 210	att Ile	ggg Gly	ggg Gly	cat His	ggg Gly 215	act Thr	act Thr	atc Ile	ggg Gly	ggg Gly 220	att Ile	att Ile	gtt Val	gac Asp	672		
tct Ser 225	ggg Gly	aag Lys	ttc Phe	cca Pro	tgg Trp 230	aag Lys	gac Asp	tac Tyr	cca Pro	gaa Glu 235	aag Lys	ttc Phe	cct Pro	caa Gln	ttc Phe 240	720		
tct Ser	caa Gln	cct Pro	gcc Ala 245	gaa Glu	gga Gly	tat Tyr	cac His	ggg Gly 250	act Thr	atc Ile	tac Tyr	aat Asn	gaa Glu	gcc Ala 255	tac Tyr	768		
ggg Gly	aac Asn	ttg Leu	gca Ala 260	tac Tyr	atc Ile	gtt Val	cat His	gtt Val 265	aga Arg	act Thr	gaa Glu	cta Leu 270	tta Leu	aga Arg	gat Asp	816		
ttg Leu	ggg Gly	cca Pro 275	ttg Leu	atg Met	aac Asn	cca Pro	ttt Phe 280	gcc Ala	tct Ser	ttc Phe	ttg Leu	cta Leu 285	cta Leu	caa Gln	ggg Gly	864		
gtt Val	gaa Glu 290	aca Thr	tta Leu	tct Ser	ttg Leu	aga Arg 295	gct Ala	gaa Glu	aga Arg	cac His	ggg Gly 300	gaa Glu	aat Asn	gca Ala	ttg Leu	912		
aag Lys 305	tta Leu	gcc Ala	aaa Lys	tgg Trp 310	tta Leu	gaa Glu	caa Gln	tcc Ser	cca Pro	tac Tyr 315	gta Val	tct Ser	tgg Trp	gtt Val	tca Ser 320	960		
tac Tyr	cct Pro	ggg Gly	tta Leu	gca Ala 325	tct Ser	cat His	tct Ser	cat His	cat His 330	gaa Glu	aat Asn	gct Ala	aag Lys	aag Lys 335	tat Tyr	1008		
cta Leu	tct Ser	aac Asn	ggg Gly 340	ttc Phe	ggg Gly	ggg Gly	gtc Val	tta Leu 345	tct Ser	ttc Phe	ggg Gly	gta Val	aaa Lys 350	gac Asp	tta Leu	1056		
cca Pro	aat Asn	gcc Ala 355	gac Asp	aag Lys	gaa Glu	act Thr	gac Asp 360	cca Pro	ttc Phe	aaa Lys	ctt Leu	tct Ser 365	ggg Gly	gct Ala	caa Gln	1104		
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Ala	Lys	Thr	Leu	Val	Ile	Ala	Pro	Tyr	Phe	Thr	Thr	His	Lys	Gln	Leu		
385					390					395				400			
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Asn	Asp	Lys	Glu	Lys	Leu	Ala	Ser	Gly	Val	Thr	Lys	Asp	Leu	Ile	Arg		
				405					410					415			
gtc	tct	gtt	ggg	atc	gaa	ttt	att	gat	gac	att	att	gca	gac	ttc	cag	1296	
Val	Ser	Val	Gly	Ile	Glu	Phe	Ile	Asp	Asp	Ile	Ile	Ala	Asp	Phe	Gln		
			420					425					430				
caa	tct	ttt	gaa	act	gtt	ttc	gct	ggc	caa	aaa	cca	tga				1335	
Gln	Ser	Phe	Glu	Thr	Val	Phe	Ala	Gly	Gln	Lys	Pro						
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<210> 48

<211> 444

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 48

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Pro	Gly	Asp	Asn	Ala	His	Arg	Ser	Arg	Ala	Val	Pro	Ile	Tyr	Ala	Thr		
			20					25					30				
Thr	Ser	Tyr	Val	Phe	Glu	Asn	Ser	Lys	His	Gly	Ser	Gln	Leu	Phe	Gly		
		35					40					45					
Leu	Glu	Val	Pro	Gly	Tyr	Val	Tyr	Ser	Arg	Phe	Gln	Asn	Pro	Thr	Ser		
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Asn	Val	Leu	Glu	Glu	Arg	Ile	Ala	Ala	Leu	Glu	Gly	Gly	Ala	Ala	Ala		
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Leu	Ala	Val	Ser	Ser	Gly	Gln	Ala	Ala	Gln	Thr	Leu	Ala	Ile	Gln	Gly		
				85					90					95			
Leu	Ala	His	Thr	Gly	Asp	Asn	Ile	Val	Ser	Thr	Ser	Tyr	Leu	Tyr	Gly		
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Gly	Thr	Tyr	Asn	Gln	Phe	Lys	Ile	Ser	Phe	Lys	Arg	Phe	Gly	Ile	Glu		
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Ala	Arg	Phe	Val	Glu	Gly	Asp	Asn	Pro	Glu	Glu	Phe	Glu	Lys	Val	Phe		
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Asp Glu Arg Thr Lys Ala Val Tyr Leu Glu Thr Ile Gly Asn Pro Lys
 145 150 155 160
 Tyr Asn Val Pro Asp Phe Glu Lys Ile Val Ala Ile Ala His Lys His
 165 170 175
 Gly Ile Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Tyr Phe
 180 185 190
 Cys Gln Pro Ile Lys Tyr Gly Ala Asp Ile Val Thr His Ser Ala Thr
 195 200 205
 Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Ile Ile Val Asp
 210 215 220
 Ser Gly Lys Phe Pro Trp Lys Asp Tyr Pro Glu Lys Phe Pro Gln Phe
 225 230 235 240
 Ser Gln Pro Ala Glu Gly Tyr His Gly Thr Ile Tyr Asn Glu Ala Tyr
 245 250 255
 Gly Asn Leu Ala Tyr Ile Val His Val Arg Thr Glu Leu Leu Arg Asp
 260 265 270
 Leu Gly Pro Leu Met Asn Pro Phe Ala Ser Phe Leu Leu Leu Gln Gly
 275 280 285
 Val Glu Thr Leu Ser Leu Arg Ala Glu Arg His Gly Glu Asn Ala Leu
 290 295 300
 Lys Leu Ala Lys Trp Leu Glu Gln Ser Pro Tyr Val Ser Trp Val Ser
 305 310 315 320
 Tyr Pro Gly Leu Ala Ser His Ser His His Glu Asn Ala Lys Lys Tyr
 325 330 335
 Leu Ser Asn Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys Asp Leu
 340 345 350
 Pro Asn Ala Asp Lys Glu Thr Asp Pro Phe Lys Leu Ser Gly Ala Gln
 355 360 365
 Val Val Asp Asn Leu Lys Leu Ala Ser Asn Leu Ala Asn Val Gly Asp
 370 375 380
 Ala Lys Thr Leu Val Ile Ala Pro Tyr Phe Thr Thr His Lys Gln Leu
 385 390 395 400
 Asn Asp Lys Glu Lys Leu Ala Ser Gly Val Thr Lys Asp Leu Ile Arg
 405 410 415

Val Ser Val Gly Ile Glu Phe Ile Asp Asp Ile Ile Ala Asp Phe Gln
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Gln Ser Phe Glu Thr Val Phe Ala Gly Gln Lys Pro
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<210> 49

<211> 1335

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> CDS

<222> (1)..(1335)

<223>

<400> 49

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Thr Ala Asp Ala His Asn Pro Arg Ala Val Pro Ile Tyr Ala Thr Thr	
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tct tac gtc ttc aac gac tct aag cat ggt gct caa ttg ttc ggt tta	144
Ser Tyr Val Phe Asn Asp Ser Lys His Gly Ala Gln Leu Phe Gly Leu	
35 40 45	

gaa act cca ggt tac att tac tct cgt att atg aac cct act cta gac	192
Glu Thr Pro Gly Tyr Ile Ser Arg Ile Met Asn Pro Thr Leu Asp	
50 55 60	

gtc ttg gaa aag aga ttg gca gcc tta gaa ggt ggt att gct gct ttg	240
Val Leu Glu Lys Arg Leu Ala Ala Leu Glu Gly Gly Ile Ala Ala Leu	
65 70 75 80	

gct act tct tct ggc caa gct gct caa acc ttg gct gtc act ggt ttg	288
Ala Thr Ser Ser Gly Gln Ala Ala Gln Thr Leu Ala Val Thr Gly Leu	
85 90 95	

gcc cac act ggt gac aat att gtc tct acc tct ttc tta tac ggt ggt	336
Ala His Thr Gly Asp Asn Ile Val Ser Thr Ser Phe Leu Tyr Gly Gly	
100 105 110	

act tat aac caa ttc aag gtt gcc ttc aag aga tta gga att gaa gct	384
Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly Ile Glu Ala	
115 120 125	

aga ttt gtc gat ggt gac aag cca gaa gac ttc gaa aag ttg ttc gat	432
Arg Phe Val Asp Gly Asp Lys Pro Glu Asp Phe Glu Lys Leu Phe Asp	
130 135 140	

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aat gtc cca gac ttc gaa aag att gtt gct gtt gct cat aag cat ggt Asn Val Pro Asp Phe Glu Lys Ile Val Ala Val Ala His Lys His Gly 165 170 175	528
atc cca gtt gtt gtt gac aac act ttc ggt gcc ggt ggt ttc ttc tgc Ile Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Phe Phe Cys 180 185 190	576
caa cct atc aaa tac ggt gct gat atc gtt act cac tct gct acc aag Gln Pro Ile Lys Tyr Gly Ala Asp Ile Val Thr His Ser Ala Thr Lys 195 200 205	624
tgg atc ggt ggt cat ggt gtc acc gtt ggt ggt gtc atc att gac tct Trp Ile Gly Gly His Gly Val Thr Val Gly Gly Val Ile Ile Asp Ser 210 215 220	672
ggt aag ttc cca tgg aag gat tac ccg gaa aag ttc cct caa ttc tct Gly Lys Phe Pro Trp Lys Asp Tyr Pro Glu Lys Phe Pro Gln Phe Ser 225 230 235 240	720
cag cca tct gaa ggt tat cat ggt ttg atc ttc aat gat gcc ttt ggt Gln Pro Ser Glu Gly Tyr His Gly Leu Ile Phe Asn Asp Ala Phe Gly 245 250 255	768
cca gct gct ttc att ggt cat gta aga acc gaa ttg cta aga gat tta Pro Ala Ala Phe Ile Gly His Val Arg Thr Glu Leu Leu Arg Asp Leu 260 265 270	816
ggt cca gtg ttg agt cca ttc gct ggt ttc ttg ttg tta cag ggt ctt Gly Pro Val Leu Ser Pro Phe Ala Gly Phe Leu Leu Leu Gln Gly Leu 275 280 285	864
gaa act ttg tct cta aga ggt gaa aga cac ggt tcc aac gct ttg aag Glu Thr Leu Ser Leu Arg Gly Glu Arg His Gly Ser Asn Ala Leu Lys 290 295 300	912
ttg gct caa tac ttg gaa agt tct cca tac gtt tca tgg gtc tct tac Leu Ala Gln Tyr Leu Glu Ser Ser Pro Tyr Val Ser Trp Val Ser Tyr 305 310 315 320	960
cca ggt ttg cca tct cac tct cac cac gaa aac gct aag aaa tac ttg Pro Gly Leu Pro Ser His Ser His His Glu Asn Ala Lys Lys Tyr Leu 325 330 335	1008
gaa aat ggt ttc ggt ggt gtt tta tcc ttc ggt gtc aaa gat ttg cct Glu Asn Gly Phe Gly Gly Val Leu Ser Phe Gly Val Lys Asp Leu Pro 340 345 350	1056
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gac gaa gaa aag tta gct tct ggt gtt acc aag gac ttg atc cgt gtt Asp Glu Glu Lys Leu Ala Ser Gly Val Thr Lys Asp Leu Ile Arg Val 405 410 415	1248

tct gtt ggt act gaa ttc att gac gac att att gct gac ttt gaa gca 1296
 Ser Val Gly Thr Glu Phe Ile Asp Asp Ile Ile Ala Asp Phe Glu Ala
 420 425 430

tct ttc gct act gtc ttc aat ggc caa aaa cct gaa taa 1335
 Ser Phe Ala Thr Val Phe Asn Gly Gln Lys Pro Glu
 435 440

<210> 50

<211> 444

<212> PRT

<213> Kluyveromyces lactis

<400> 50

Met Pro Ser His Phe Asp Thr Leu Gln Leu His Ala Gly Gln Glu Lys
 1 5 10 15

Thr Ala Asp Ala His Asn Pro Arg Ala Val Pro Ile Tyr Ala Thr Thr
 20 25 30

Ser Tyr Val Phe Asn Asp Ser Lys His Gly Ala Gln Leu Phe Gly Leu
 35 40 45

Glu Thr Pro Gly Tyr Ile Tyr Ser Arg Ile Met Asn Pro Thr Leu Asp
 50 55 60

Val Leu Glu Lys Arg Leu Ala Ala Leu Glu Gly Gly Ile Ala Ala Leu
 65 70 75 80

Ala Thr Ser Ser Gly Gln Ala Ala Gln Thr Leu Ala Val Thr Gly Leu
 85 90 95

Ala His Thr Gly Asp Asn Ile Val Ser Thr Ser Phe Leu Tyr Gly Gly
 100 105 110

Thr Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly Ile Glu Ala
 115 120 125

Arg Phe Val Asp Gly Asp Lys Pro Glu Asp Phe Glu Lys Leu Phe Asp
 130 135 140

Glu Lys Thr Lys Ala Leu Tyr Leu Glu Ser Ile Gly Asn Pro Lys Tyr
 145 150 155 160

Asn Val Pro Asp Phe Glu Lys Ile Val Ala Val Ala His Lys His Gly
 165 170 175

Ile Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Phe Phe Cys

180					185					190					
Gln	Pro	Ile	Lys	Tyr	Gly	Ala	Asp	Ile	Val	Thr	His	Ser	Ala	Thr	Lys
		195					200					205			
Trp	Ile	Gly	Gly	His	Gly	Val	Thr	Val	Gly	Gly	Val	Ile	Ile	Asp	Ser
	210					215					220				
Gly	Lys	Phe	Pro	Trp	Lys	Asp	Tyr	Pro	Glu	Lys	Phe	Pro	Gln	Phe	Ser
225					230					235					240
Gln	Pro	Ser	Glu	Gly	Tyr	His	Gly	Leu	Ile	Phe	Asn	Asp	Ala	Phe	Gly
				245					250					255	
Pro	Ala	Ala	Phe	Ile	Gly	His	Val	Arg	Thr	Glu	Leu	Leu	Arg	Asp	Leu
			260					265					270		
Gly	Pro	Val	Leu	Ser	Pro	Phe	Ala	Gly	Phe	Leu	Leu	Leu	Gln	Gly	Leu
		275					280					285			
Glu	Thr	Leu	Ser	Leu	Arg	Gly	Glu	Arg	His	Gly	Ser	Asn	Ala	Leu	Lys
	290					295					300				
Leu	Ala	Gln	Tyr	Leu	Glu	Ser	Ser	Pro	Tyr	Val	Ser	Trp	Val	Ser	Tyr
305					310					315					320
Pro	Gly	Leu	Pro	Ser	His	Ser	His	His	Glu	Asn	Ala	Lys	Lys	Tyr	Leu
				325					330					335	
Glu	Asn	Gly	Phe	Gly	Gly	Val	Leu	Ser	Phe	Gly	Val	Lys	Asp	Leu	Pro
			340					345					350		
Asn	Ala	Ser	Glu	Glu	Ser	Asp	Pro	Phe	Lys	Ala	Ser	Gly	Ala	Gln	Val
		355					360					365			
Val	Asp	Asn	Leu	Lys	Leu	Ala	Ser	Asn	Leu	Ala	Asn	Val	Gly	Asp	Ser
	370					375					380				
Lys	Thr	Leu	Val	Ile	Ala	Pro	Tyr	Phe	Thr	Thr	His	Gln	Gln	Leu	Thr
385					390					395					400
Asp	Glu	Glu	Lys	Leu	Ala	Ser	Gly	Val	Thr	Lys	Asp	Leu	Ile	Arg	Val
				405					410					415	
Ser	Val	Gly	Thr	Glu	Phe	Ile	Asp	Asp	Ile	Ile	Ala	Asp	Phe	Glu	Ala
			420					425					430		
Ser	Phe	Ala	Thr	Val	Phe	Asn	Gly	Gln	Lys	Pro	Glu				
		435					440								

<210> 51
 <211> 1323
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(1323)
 <223>

<400> 51
 atg cct tct cac ttt gat aca ctt caa tta cat gct ggt caa cca gtt 48
 Met Pro Ser His Phe Asp Thr Leu Gln Leu His Ala Gly Gln Pro Val
 1 5 10 15
 gaa aaa cca cac caa cca aga gcc cca cca att tat gca acc acc tcc 96
 Glu Lys Pro His Gln Pro Arg Ala Pro Pro Ile Tyr Ala Thr Thr Ser
 20 25 30
 tat gtt ttc aat gac tct aaa cac ggt gct caa tta ttt ggt tta gaa 144
 Tyr Val Phe Asn Asp Ser Lys His Gly Ala Gln Leu Phe Gly Leu Glu
 35 40 45
 acc cca gga tac att tac tcc aga att atg aat cca aca aac gat gtg 192
 Thr Pro Gly Tyr Ile Tyr Ser Arg Ile Met Asn Pro Thr Asn Asp Val
 50 55 60
 ttt gaa caa aga att gct gcc ttg gaa ggt ggt att ggt gca ttg gcc 240
 Phe Glu Gln Arg Ile Ala Ala Leu Glu Gly Gly Ile Gly Ala Leu Ala
 65 70 75 80
 act tct tct ggt caa tca gct caa ttc ttg gcc att gct ggg ttg gct 288
 Thr Ser Ser Gly Gln Ser Ala Gln Phe Leu Ala Ile Ala Gly Leu Ala
 85 90 95
 cat gct ggt gat aac att atc agt aca tcc tac ttg tat ggt ggt act 336
 His Ala Gly Asp Asn Ile Ile Ser Thr Ser Tyr Leu Tyr Gly Gly Thr
 100 105 110
 tat aat caa ttc aaa gtt gct ttc aaa cgt ttg ggc att gaa acc aaa 384
 Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly Ile Glu Thr Lys
 115 120 125
 ttc gtt aat ggt gac gcc gct gaa gat ttt gct aaa ttg att gac gac 432
 Phe Val Asn Gly Asp Ala Ala Glu Asp Phe Ala Lys Leu Ile Asp Asp
 130 135 140
 aag aca aaa gct att tat att gaa acc att gga aac cct aaa tat aat 480
 Lys Thr Lys Ala Ile Tyr Ile Glu Thr Ile Gly Asn Pro Lys Tyr Asn
 145 150 155 160
 gtt ccg gac ttt gaa aaa atc acc aaa ttg gcc cat gaa cac ggt att 528
 Val Pro Asp Phe Glu Lys Ile Thr Lys Leu Ala His Glu His Gly Ile
 165 170 175
 cct gtt gtt gtc gac aac act ttt ggt gct ggt gga ttt tta gtt aac 576
 Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Phe Leu Val Asn

180				185				190								
cca	att	gcc	cac	ggt	gct	gat	att	gtt	gtt	cat	tct	gct	act	aaa	tgg	624
Pro	Ile	Ala	His	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Ala	Thr	Lys	Trp	
		195					200					205				
att	ggt	ggt	cac	ggt	act	aca	att	gct	ggt	gtt	att	gtt	gat	tcc	ggt	672
Ile	Gly	Gly	His	Gly	Thr	Thr	Ile	Ala	Gly	Val	Ile	Val	Asp	Ser	Gly	
	210						215				220					
aac	ttc	cca	tgg	acc	gag	tac	cca	gaa	aaa	tac	cca	caa	ttc	tct	aaa	720
Asn	Phe	Pro	Trp	Thr	Glu	Tyr	Pro	Glu	Lys	Tyr	Pro	Gln	Phe	Ser	Lys	
225					230					235					240	
cca	tca	gaa	ggt	tac	cac	ggg	ttg	atc	ttg	aat	gat	gct	tta	ggt	aag	768
Pro	Ser	Glu	Gly	Tyr	His	Gly	Leu	Ile	Leu	Asn	Asp	Ala	Leu	Gly	Lys	
				245					250					255		
gcc	gca	tac	att	ggt	cac	ttg	aga	att	gaa	ttg	ttg	aga	gac	ttg	ggt	816
Ala	Ala	Tyr	Ile	Gly	His	Leu	Arg	Ile	Glu	Leu	Leu	Arg	Asp	Leu	Gly	
			260					265					270			
cca	gct	ttg	aat	cca	ttt	gga	agt	ttt	ttg	ttg	ttg	caa	ggt	tta	gaa	864
Pro	Ala	Leu	Asn	Pro	Phe	Gly	Ser	Phe	Leu	Leu	Leu	Gln	Gly	Leu	Glu	
		275					280					285				
act	ttg	tct	ttg	aga	gtt	gaa	aga	caa	tct	gaa	aat	gct	ttg	aaa	ttg	912
Thr	Leu	Ser	Leu	Arg	Val	Glu	Arg	Gln	Ser	Glu	Asn	Ala	Leu	Lys	Leu	
	290					295					300					
gcc	caa	tgg	ttg	gaa	aag	aac	cca	aat	gtt	gag	tct	gtg	tcc	tat	ttg	960
Ala	Gln	Trp	Leu	Glu	Lys	Asn	Pro	Asn	Val	Glu	Ser	Val	Ser	Tyr	Leu	
305					310					315					320	
gga	ttg	cca	tct	cac	gaa	tcc	cac	gaa	ttg	agt	aaa	aaa	tac	ttg	aac	1008
Gly	Leu	Pro	Ser	His	Glu	Ser	His	Glu	Leu	Ser	Lys	Lys	Tyr	Leu	Asn	
				325					330					335		
aat	gac	gct	aag	tac	ttt	ggt	ggt	gct	tta	gca	ttt	act	gtc	aag	gac	1056
Asn	Asp	Ala	Lys	Tyr	Phe	Gly	Gly	Ala	Leu	Ala	Phe	Thr	Val	Lys	Asp	
			340					345					350			
atc	acc	aac	acc	tcc	agc	gac	cca	ttc	aat	gaa	gcc	tca	cca	aag	ttg	1104
Ile	Thr	Asn	Thr	Ser	Ser	Asp	Pro	Phe	Asn	Glu	Ala	Ser	Pro	Lys	Leu	
		355					360					365				
gtt	gac	aat	ttg	gag	att	gct	tca	aac	ttg	gct	aat	gtg	ggt	gac	tct	1152
Val	Asp	Asn	Leu	Glu	Ile	Ala	Ser	Asn	Leu	Ala	Asn	Val	Gly	Asp	Ser	
	370					375					380					
aag	act	ttg	gtt	att	gct	cca	tgg	ttt	act	aca	cat	caa	caa	ttg	tct	1200
Lys	Thr	Leu	Val	Ile	Ala	Pro	Trp	Phe	Thr	Thr	His	Gln	Gln	Leu	Ser	
385					390					395					400	
gat	gaa	gaa	aag	ttg	gct	tct	ggt	gtt	acc	aag	ggc	tta	atc	aga	gtt	1248
Asp	Glu	Glu	Lys	Leu	Ala	Ser	Gly	Val	Thr	Lys	Gly	Leu	Ile	Arg	Val	
				405					410					415		
tct	act	ggt	act	gaa	tat	att	gat	gat	att	att	aac	gac	ttt	gaa	caa	1296
Ser	Thr	Gly	Thr	Glu	Tyr	Ile	Asp	Asp	Ile	Ile	Asn	Asp	Phe	Glu	Gln	
			420					425					430			
gca	ttc	aag	aag	gtt	tat	aac	aac	taa								1323
Ala	Phe	Lys	Lys	Val	Tyr	Asn	Asn									
		435					440									

<210> 52

<211> 440

<212> PRT

<213> Candida albicans

<400> 52

Met Pro Ser His Phe Asp Thr Leu Gln Leu His Ala Gly Gln Pro Val
 1 5 10 15

Glu Lys Pro His Gln Pro Arg Ala Pro Pro Ile Tyr Ala Thr Thr Ser
 20 25 30

Tyr Val Phe Asn Asp Ser Lys His Gly Ala Gln Leu Phe Gly Leu Glu
 35 40 45

Thr Pro Gly Tyr Ile Tyr Ser Arg Ile Met Asn Pro Thr Asn Asp Val
 50 55 60

Phe Glu Gln Arg Ile Ala Ala Leu Glu Gly Gly Ile Gly Ala Leu Ala
 65 70 75 80

Thr Ser Ser Gly Gln Ser Ala Gln Phe Leu Ala Ile Ala Gly Leu Ala
 85 90 95

His Ala Gly Asp Asn Ile Ile Ser Thr Ser Tyr Leu Tyr Gly Gly Thr
 100 105 110

Tyr Asn Gln Phe Lys Val Ala Phe Lys Arg Leu Gly Ile Glu Thr Lys
 115 120 125

Phe Val Asn Gly Asp Ala Ala Glu Asp Phe Ala Lys Leu Ile Asp Asp
 130 135 140

Lys Thr Lys Ala Ile Tyr Ile Glu Thr Ile Gly Asn Pro Lys Tyr Asn
 145 150 155 160

Val Pro Asp Phe Glu Lys Ile Thr Lys Leu Ala His Glu His Gly Ile
 165 170 175

Pro Val Val Val Asp Asn Thr Phe Gly Ala Gly Gly Phe Leu Val Asn
 180 185 190

Pro Ile Ala His Gly Ala Asp Ile Val Val His Ser Ala Thr Lys Trp
 195 200 205

Ile Gly Gly His Gly Thr Thr Ile Ala Gly Val Ile Val Asp Ser Gly
 210 215 220

Asn Phe Pro Trp Thr Glu Tyr Pro Glu Lys Tyr Pro Gln Phe Ser Lys
 225 230 235 240

Pro Ser Glu Gly Tyr His Gly Leu Ile Leu Asn Asp Ala Leu Gly Lys
 245 250 255

Ala Ala Tyr Ile Gly His Leu Arg Ile Glu Leu Leu Arg Asp Leu Gly
 260 265 270

Pro Ala Leu Asn Pro Phe Gly Ser Phe Leu Leu Leu Gln Gly Leu Glu
 275 280 285

Thr Leu Ser Leu Arg Val Glu Arg Gln Ser Glu Asn Ala Leu Lys Leu
 290 295 300

Ala Gln Trp Leu Glu Lys Asn Pro Asn Val Glu Ser Val Ser Tyr Leu
 305 310 315 320

Gly Leu Pro Ser His Glu Ser His Glu Leu Ser Lys Lys Tyr Leu Asn
 325 330 335

Asn Asp Ala Lys Tyr Phe Gly Gly Ala Leu Ala Phe Thr Val Lys Asp
 340 345 350

Ile Thr Asn Thr Ser Ser Asp Pro Phe Asn Glu Ala Ser Pro Lys Leu
 355 360 365

Val Asp Asn Leu Glu Ile Ala Ser Asn Leu Ala Asn Val Gly Asp Ser
 370 375 380

Lys Thr Leu Val Ile Ala Pro Trp Phe Thr Thr His Gln Gln Leu Ser
 385 390 395 400

Asp Glu Glu Lys Leu Ala Ser Gly Val Thr Lys Gly Leu Ile Arg Val
 405 410 415

Ser Thr Gly Thr Glu Tyr Ile Asp Asp Ile Ile Asn Asp Phe Glu Gln
 420 425 430

Ala Phe Lys Lys Val Tyr Asn Asn
 435 440

<210> 53

<211> 1290

<212> DNA

<213> Schizosaccharomyces pombe

<220>

<221> CDS

<222> (1)..(1290)

<223>

<400> 53

atg cca gtc gag agt gaa cat ttc gaa act tta caa tta cat gct ggc	48
Met Pro Val Glu Ser Glu His Phe Glu Thr Leu Gln Leu His Ala Gly	
1 5 10 15	
caa gag cct gat gct gct acc agc tct cgt gcc gtt ccc atc tac gct	96
Gln Glu Pro Asp Ala Ala Thr Ser Ser Arg Ala Val Pro Ile Tyr Ala	
20 25 30	
act act tcc tat gtt ttc cgt gat tgc gac cat ggc ggc cgc ttg ttc	144
Thr Thr Ser Tyr Val Phe Arg Asp Cys Asp His Gly Gly Arg Leu Phe	
35 40 45	
gga tta cag gaa cca ggt tac atc tac tcg cgt atg atg aat ccc acc	192
Gly Leu Gln Glu Pro Gly Tyr Ile Tyr Ser Arg Met Met Asn Pro Thr	
50 55 60	
gcc gac gtt ttt gag aaa cgt att gcc gcc ttg gag cat ggc gct gct	240
Ala Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu His Gly Ala Ala	
65 70 75 80	
gca atc gct act agt tcc ggt act tcc gct ctc ttc atg gct ttg acc	288
Ala Ile Ala Thr Ser Ser Gly Thr Ser Ala Leu Phe Met Ala Leu Thr	
85 90 95	
acg ttg gct aag gcc ggt gat aac att gtc tcc act tct tac ctt tat	336
Thr Leu Ala Lys Ala Gly Asp Asn Ile Val Ser Thr Ser Tyr Leu Tyr	
100 105 110	
ggt ggt act tac aac ctc ttc aag gtt acc ctg cct aga ttg gga att	384
Gly Gly Thr Tyr Asn Leu Phe Lys Val Thr Leu Pro Arg Leu Gly Ile	
115 120 125	
act acc aag ttt gtc aat ggt gat gat cct aat gat ctt gca gct cag	432
Thr Thr Lys Phe Val Asn Gly Asp Asp Pro Asn Asp Leu Ala Ala Gln	
130 135 140	
att gat gaa aac aca aag gct gtt tac gtt gag tcc atc ggc aat ccc	480
Ile Asp Glu Asn Thr Lys Ala Val Tyr Val Glu Ser Ile Gly Asn Pro	
145 150 155 160	
atg tac aac gtt ccc gat ttt gag cgt atc gct gag gtt gct cat gcc	528
Met Tyr Asn Val Pro Asp Phe Glu Arg Ile Ala Glu Val Ala His Ala	
165 170 175	
gct ggt gtg cct tta atg gtc gat aac act ttt ggc ggc ggt ggt tat	576
Ala Gly Val Pro Leu Met Val Asp Asn Thr Phe Gly Gly Gly Tyr	
180 185 190	
ttg gtt cgt ccc att gac cac ggt gcc gat atc gtt acc cac tct gcc	624
Leu Val Arg Pro Ile Asp His Gly Ala Asp Ile Val Thr His Ser Ala	
195 200 205	
act aag tgg atc ggt ggt cat ggc act act att ggc ggt gtg att gtt	672
Thr Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Val Ile Val	
210 215 220	

gat agt ggt aag ttt gac tgg aag aag aac agc aag cgt ttc cct gaa	720
Asp Ser Gly Lys Phe Asp Trp Lys Lys Asn Ser Lys Arg Phe Pro Glu	
225 230 235 240	
ttc aac gag cct cat ccc ggt tac cat ggc atg gtc ttt act gaa act	768
Phe Asn Glu Pro His Pro Gly Tyr His Gly Met Val Phe Thr Glu Thr	
245 250 255	
ttt ggt aac ttg gca tat gct ttt gct tgc cgt act caa act ctc cgt	816
Phe Gly Asn Leu Ala Tyr Ala Phe Ala Cys Arg Thr Gln Thr Leu Arg	
260 265 270	
gat gtt ggt ggc aat gcc aat cca ttc ggt gtc ttt ttg ctt ctt caa	864
Asp Val Gly Gly Asn Ala Asn Pro Phe Gly Val Phe Leu Leu Leu Gln	
275 280 285	
ggt ctt gaa acg ctt tct ctt cgt atg gag cgt cac gtt caa aat gca	912
Gly Leu Glu Thr Leu Ser Leu Arg Met Glu Arg His Val Gln Asn Ala	
290 295 300	
ttt gct ctt gca aaa tat ttg gaa aag cac ccc aag gtt aac tgg gtt	960
Phe Ala Leu Ala Lys Tyr Leu Glu Lys His Pro Lys Val Asn Trp Val	
305 310 315 320	
tct tac cct ggt ctt gaa tct cac gtc tct cac aaa ctt gcc aag aag	1008
Ser Tyr Pro Gly Leu Glu Ser His Val Ser His Lys Leu Ala Lys Lys	
325 330 335	
tac ttg aaa aat ggt tac ggc gcc gtt ctc agc ttt ggc gct aaa ggt	1056
Tyr Leu Lys Asn Gly Tyr Gly Ala Val Leu Ser Phe Gly Ala Lys Gly	
340 345 350	
ggc cct gat caa agt cgt aag gta gtc aat gcc tta aag ctt gct agt	1104
Gly Pro Asp Gln Ser Arg Lys Val Val Asn Ala Leu Lys Leu Ala Ser	
355 360 365	
cag ttg gcc aat gtt ggt gat gcc aaa act ttg gtt atc gct cct gcc	1152
Gln Leu Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile Ala Pro Ala	
370 375 380	
tat acc act cat tta caa tta act gat gag gag caa att tct gcc ggt	1200
Tyr Thr Thr His Leu Gln Leu Thr Asp Glu Glu Gln Ile Ser Ala Gly	
385 390 395 400	
gtc act aag gat ctt att cgt gtg gcc gtc ggt att gag cac atc gat	1248
Val Thr Lys Asp Leu Ile Arg Val Ala Val Gly Ile Glu His Ile Asp	
405 410 415	
gat att atc gcc gac ttt gct caa gct ttg gaa gtt gcc taa	1290
Asp Ile Ile Ala Asp Phe Ala Gln Ala Leu Glu Val Ala	
420 425	

<210> 54

<211> 429

<212> PRT

<213> Schizosaccharomyces pombe

<400> 54

Met Pro Val Glu Ser Glu His Phe Glu Thr Leu Gln Leu His Ala Gly
1 5 10 15

Gln Glu Pro Asp Ala Ala Thr Ser Ser Arg Ala Val Pro Ile Tyr Ala
 20 25 30
 Thr Thr Ser Tyr Val Phe Arg Asp Cys Asp His Gly Gly Arg Leu Phe
 35 40 45
 Gly Leu Gln Glu Pro Gly Tyr Ile Tyr Ser Arg Met Met Asn Pro Thr
 50 55 60
 Ala Asp Val Phe Glu Lys Arg Ile Ala Ala Leu Glu His Gly Ala Ala
 65 70 75 80
 Ala Ile Ala Thr Ser Ser Gly Thr Ser Ala Leu Phe Met Ala Leu Thr
 85 90 95
 Thr Leu Ala Lys Ala Gly Asp Asn Ile Val Ser Thr Ser Tyr Leu Tyr
 100 105 110
 Gly Gly Thr Tyr Asn Leu Phe Lys Val Thr Leu Pro Arg Leu Gly Ile
 115 120 125
 Thr Thr Lys Phe Val Asn Gly Asp Asp Pro Asn Asp Leu Ala Ala Gln
 130 135 140
 Ile Asp Glu Asn Thr Lys Ala Val Tyr Val Glu Ser Ile Gly Asn Pro
 145 150 155 160
 Met Tyr Asn Val Pro Asp Phe Glu Arg Ile Ala Glu Val Ala His Ala
 165 170 175
 Ala Gly Val Pro Leu Met Val Asp Asn Thr Phe Gly Gly Gly Gly Tyr
 180 185 190
 Leu Val Arg Pro Ile Asp His Gly Ala Asp Ile Val Thr His Ser Ala
 195 200 205
 Thr Lys Trp Ile Gly Gly His Gly Thr Thr Ile Gly Gly Val Ile Val
 210 215 220
 Asp Ser Gly Lys Phe Asp Trp Lys Lys Asn Ser Lys Arg Phe Pro Glu
 225 230 235 240
 Phe Asn Glu Pro His Pro Gly Tyr His Gly Met Val Phe Thr Glu Thr
 245 250 255
 Phe Gly Asn Leu Ala Tyr Ala Phe Ala Cys Arg Thr Gln Thr Leu Arg
 260 265 270
 Asp Val Gly Gly Asn Ala Asn Pro Phe Gly Val Phe Leu Leu Leu Gln

275

280

285

Gly Leu Glu Thr Leu Ser Leu Arg Met Glu Arg His Val Gln Asn Ala
 290 295 300

Phe Ala Leu Ala Lys Tyr Leu Glu Lys His Pro Lys Val Asn Trp Val
 305 310 315 320

Ser Tyr Pro Gly Leu Glu Ser His Val Ser His Lys Leu Ala Lys Lys
 325 330 335

Tyr Leu Lys Asn Gly Tyr Gly Ala Val Leu Ser Phe Gly Ala Lys Gly
 340 345 350

Gly Pro Asp Gln Ser Arg Lys Val Val Asn Ala Leu Lys Leu Ala Ser
 355 360 365

Gln Leu Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile Ala Pro Ala
 370 375 380

Tyr Thr Thr His Leu Gln Leu Thr Asp Glu Glu Gln Ile Ser Ala Gly
 385 390 395 400

Val Thr Lys Asp Leu Ile Arg Val Ala Val Gly Ile Glu His Ile Asp
 405 410 415

Asp Ile Ile Ala Asp Phe Ala Gln Ala Leu Glu Val Ala
 420 425

<210> 55

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 55

cccgggatcc gctagcggcg cgccggcccg cccggtgtga aataccgcac ag

52

<210> 56

<211> 53

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 56

tctagactcg agcggccgcg gccggccttt aaattgaaga cgaaagggcc tcg

53

<210> 57

<211> 47

<212> DNA

<213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer
 <400> 57
 gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 58
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer
 <400> 58
 gagaggcgcg ccgctagcgt gggcgaagaa ctccagca 38

<210> 59
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer
 <400> 59
 gagagggcgg ccgcgcaaag tcccgttcg tgaa 34

<210> 60
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer
 <400> 60
 gagagggcgg ccgctcaagt cggcgaagcc acgc 34

<210> 61
 <211> 140
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer
 <400> 61
 tcgaatttaa atctcgagag gcctgacgtc gggcccggta ccacgcgtca tatgactagt 60
 tcggacctag ggatatcgtc gacatcgatg ctcttctgcg ttaattaaca attgggatcc 120
 tctagaccgc ggatttaaatt 140

<210> 62
 <211> 140
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer
 <400> 62


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gatcatttaa atccccgggc tagaggatcc caattgttaa ttaacgcaga agagcatcga 60
tgtcgacgat atccctaggt ccgaactagt catatgacgc gtggtaccgg gcccgacgtc 120
aggcctctcg agattttaat

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<210> 63
<211> 33
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:PCR primer

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<400> 63
gagagcggcc gccgatcctt ttttaacccat cac

```

33

```

<210> 64
<211> 32
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:PCR primer

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<400> 64
aggagcggcc gccatcggca ttttcttttg cg

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32

```

<210> 65
<211> 5091
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:plasmid

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<400> 65
gccgcgactg ccttcgcgaa gccttgcccc gcggaatttt cctccaccga gttcgtgcac 60
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<210> 66
<211> 4323
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence:plasmid

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<400> 66

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<210> 67
<211> 35
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence: PCR primer

```

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<400> 67
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```

```

<210> 68
<211> 34
<212> DNA
<213> Artificial sequence

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```

<220>
<223> Description of the artificial sequence: PCR primer

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<400> 68
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```

```

<210> 69
<211> 5860
<212> DNA
<213> Artificial sequence

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```

<220>
<223> Description of the artificial sequence: plasmid

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<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence: PCR primer

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<400> 70
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<210> 71
<211> 38
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of the artificial sequence: PCR primer

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<400> 71
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<212> DNA
<213> LysC mutant
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gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp 35 40 45	144
gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg 50 55 60	192
gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu 65 70 75 80	240
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tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn 210 215 220	672
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 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
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 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
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 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
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 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Arg Ala
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 405 410 415
 gca ggc acc gga cgc taa 1266
 Ala Gly Thr Gly Arg
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<210> 73
 <211> 421
 <212> PRT
 <213> LysC mutant

<400> 73

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35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
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 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
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 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
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 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
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 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
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 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
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 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
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 Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr

325

330

335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
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Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
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Ala Gly Thr Gly Arg
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 <211> 5860
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: plasmid

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<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

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<220>
<223> Description of the artificial sequence: PCR primer

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<213> Artificial sequence

<220>
<223> Description of the artificial sequence: PCR primer

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